

75108

Delaval, Jan

From: Liu, Samuel
Sent: Friday, September 06, 2002 9:40 AM
To: Delaval, Jan
Subject: 09/806382

09/806382 ✓

Hello, Jan,

Please search the following polypeptide sequences for 09/806382:

SEQ ID NOs: 1 and 2.

Have a great weekend!

Very best,

Samuel Wei Liu
Unit 1653
CM1 9D08
Mailbox 9B01
Tel: 306-3483

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
ian.delaval@uspto.gov

22

1

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
 Reference Librarian
 Biotechnology & Chemical Library
 CM1 1E07 - 703-308-4498
 jan.delaval@uspto.gov

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Phone #: <u>4458</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>9/19/02</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>9/12/02</u>	Litigation _____	Lexis/Nexis <input checked="" type="checkbox"/>
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>15</u>	Other _____	Other (specify) _____

OM of: US-09-806-382a-2 to: PIR_71.* out_format : pfs
Date: Sep 9, 2002 3:12 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-MODEL-frame.n2p.model -DEV-xlp  
-O=/cgml1/USPTO/spool/US09806382/runat_09092002.143848.15421/arp-query.fasta.1.752  
-DB=PIR_71 -FMT=fasta -SUFFIX=pr -GAOP=12.000 -GAPEXT=4.000  
-MIMATCH=0.100 -LOOPT=0.000 -LOOPT=0.000 -GAOP=4.500  
-GAPEXT=0.050 -XGAOP=10.000 -XGAPEXT=0.500 -FGAOP=6.000  
-FGAPEXT=7.000 -YGAOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELX=7.000 -START=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-ALIGN=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500  
-MINLEN=0 -MAXLEN=2000000000 -USER=US09806382.@cgml1.1155  
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30  
-NO_XLPHY -WAIT -THREADS=1
```

Search information block:

Query: US-09-806-382a-2
Query Length: 345
Database: PIR_71.*
Database sequences: 283138
Database length: 96089334
Search time (sec): 60.920000

Sequence	Strd Orig	%Score	Escore	Len	Documentation
pir1:A42628	+	378.50	689.71	2.1e-30	122 calgranulin B - bovine (fragment)
pir1:JUN068	+	355.31	648.31	4.5e-28	113 calgranulin B - rat
pir1:S68242	+	329.50	600.76	2.0e-25	113 calgranulin B - mouse
pir2:JC4712	+	214.50	392.47	1.0e-13	92 S-100 calcium-binding protein A1
pir2:A55406	+	213.50	390.47	1.0e-13	92 calgranulin c - pig
pir1:BCBUTR	+	177.50	324.55	6.0e-10	92 S-100 protein beta chain [valida
pir2:AA8015	+	176.50	322.81	7.6e-10	91 S-100 protein beta chain - bovin
pir1:S33985	+	176.50	322.72	7.6e-10	92 S-100 protein beta chain - mouse
pir2:A26557	+	176.50	322.44	7.6e-10	92 S-100 protein alpha chain - west
pir2:S24146	+	165.50	302.33	1.5e-09	92 S-100 protein alpha chain - rat
pir1:BCBORA	+	161.50	295.10	2.6e-08	94 S-100 protein P - human
pir2:AA1988	+	160.50	293.28	3.2e-08	94 S-100 protein alpha chain - bovi
pir2:AA5135	+	156.50	285.61	8.3e-08	98 S-100 calcium-binding protein A2
pir2:A30129	+	153.50	280.21	1.7e-07	97 profilaggrin - human (fragment)
pir1:J01300	+	153.50	280.21	1.7e-07	97 S-100 protein, lung - bovine
pir2:AA8219	+	150.50	274.38	3.4e-07	101 calgizartin - rabbit
pir1:137080	+	148.50	272.22	4.3e-07	105 calvasculin - human
pir2:166861	+	148.00	279.96	4.4e-07	38 calgizartin - human
pir2:S06207	+	147.00	271.63	4.8e-07	101 macrophage migration inhibitory
pir2:AS3217	+	147.00	268.06	7.7e-07	100 calvasculin - mouse
pir1:156163	+	146.50	268.14	8.6e-07	89 placental calcium-binding prote
pir1:JUN0685	+	140.50	259.00	2.8e-06	89 calgranulin A - mouse
pir2:S01759	+	140.00	255.17	4.0e-06	101 calvasculin - rat
pir2:BA8219	+	139.00	252.62	5.1e-06	110 S-100 calcium-binding protein A
pir2:AA8118	+	139.00	243.90	5.6e-06	306 major epidermal calcium-binding
pir2:JC5064	+	138.00	251.77	6.3e-06	98 S-100 calcium-binding protein A1
pir1:S27011	+	137.50	251.59	7.1e-06	90 calgizartin - rabbit
pir2:B28363	+	135.00	247.01	1.3e-05	90 calgizartin - rat
pir2:J00330	+	133.00	239.51	1.6e-05	217 26-Kda Ca2+-binding protein, p2
pir2:AA4314	+	133.00	243.28	1.6e-05	89 calgizartin - mouse
pir1:BCBUTR	+	133.00	245.18	1.6e-05	90 calgizartin - human
pir2:JH0663	+	128.00	233.57	6.6e-05	97 calgizartin I light chain - chick
pir2:AA8489	+	128.00	233.57	6.6e-05	97 calgizartin I light chain - mouse
pir2:JC5065	+	127.00	231.66	8.4e-05	98 calgizartin I light chain - pig
pir1:JH0310	+	123.00	224.61	0.0002	95 calgizartin I light chain - human
pir2:J01139	+	123.00	224.43	0.0002	97 calgizartin I light chain - human
pir2:B28489	+	123.00	224.43	0.0002	97 calgizartin I light chain - bovine

seq_name: pir1:A42628
seq_documentation_block:
calgranulin B - bovine (fragment)
N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory fa
in 2
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997
C:Accession: B22309; A42628
R:Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Ch
submitted to the Protein Sequence Database, July 1992
A:Reference number: A22309
A:Accession: B22309
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-122 <TAN>
R:Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.
Biochemistry 31, 5898-5905, 1992
A:Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutro
A:Reference number: A42628; M0ID:92304974
A:Accession: A42628
A:Molecule type: protein
A:Residues: 4-32, F, 34-56 <DIA>
C:Complex: heterodimer and higher complexes with calgranulin A
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; p
F:50-82/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>

alignment_scores:

Quality:	378.50	Length:	109
Ratio:	4.027	Gaps:	1
Percent Similarity:	86.239	Percent Identity:	69.725

alignment_block:

US-09-806-382a-2 x A42628 ..

Align seg 1/1 to: A42628 from: 1 to: 122

```
13 ATGTGCGAGCTGAGACGACATGAGACCATGATGACACTTCCACCA 62
|||||.....|
1 Metserdlmetgluserllegluthlilelslslnlephetlsgl 17
63 ATATCTGTGTAAGCTGGGCGACCCAGACACCTGAAACGAGGGAATTCA 112
|||||.....|
17 ntyrservalargleuglyhstyrasprhrlleuileglnlysgluserl 34
113 AAGGCGTGTGCGGAAAGATCGCAAAATTTCTCAAGAAAGGATTAAG 162
|||||.....|
34 ysglnleuvalglhlysglnleuprthleuileuylslysglnlysls 50
163 AATGAAAGGCTCATGAGACATCATGAGAGACTGAGACAAATGACAA 212
|||||.....|
51 AAGGGLAAlaIlelslsnglilemetgluAspIleAspThrAsnValAs 67
213 CAAGCAAGCTGAGCTTGAGAGAGTTCATCATGCTGATGCGAGGCTTAACST 262
|||||.....|
67 ptyrsglnleuSerPhelgluIuphrlleuileuValAlaIArgleuthly 84
263 GGGCGTCCCGGAGAGATGACAGAG...GGGAGACGAGGCGCTGGCGAC 309
|||||.....|
84 alaIAspThrIlelslsnglileuileuIleAsnThrAlaIArgleuthly 100
310 CASCATTAAGCCAGGCTGCGGAGGAGGCG 336
|||||.....|
101 ArgnllelglpIrobltyrleuIlysgly 109
```

seq_name: p1r1:JN0686

seq_documentation_block:

calgranulin B - rat
N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 23-May-1997 #text_change 22-Jun-1999
C:Accession: JN0686
R:Manatich, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.
Biochem. Biophys. Res. Commun. 194, 819-825, 1993
A:Title: Expression and cloning of migration inhibitory factor-related protein (MRP) 8 and
A:Reference number: JN0685; MUID:93434942
A:Accession: JN0686
A:Molecule type: mRNA
A:Residues: 1-113 <RNA>
A:Cross-references: GB:L18948; NID:9488156; PIDN:AAA18214.1; PID:9488157
C:Genetics:
A:Gene: MRP14
C:Complex: heterodimer and higher complexes with calgranulin A
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation; F
F:2-113/Product: calgranulin B #status predicted <MAT>
F:11-45/Domain: calmodulin repeat homology <EF1>
F:55-87/Domain: calmodulin repeat homology <EF2>
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F:80-91/Disulfide bonds: #status predicted

alignment_scores:

Quality: 355.50 Length: 107
Ratio: 3.864 Gaps: 1
Percent Similarity: 85.981 Percent Identity: 64.486

alignment_block:

US-09-806-382a-2 x JN0686 ..

Align seg 1/1 to: JN0686 from: 1 to: 113

```
16 TCGCAGCTGAGCGACATGAGACATCATCAACACCTTCACCAATA 65
|||||
7 SerGlnLeuGluArgSerIleSerThrIleIleAsnValPheHisGlnTy 23
66 CTCTGTGAGCTGGGGCCAGACACCTGACACCGAGGGGAATTCAG 115
|||||
23 rSerArgLysTyrGlnHisProAspThrLeuAsnLysAlaGluPheLysG 40
116 AGCTGTGCGAAAGATCTGCAAAATTTTCTGAAGAGAGATTAAGAT 165
|||||
40 IuMetValAlaAsnLysAspLeuProAsnPheLeuLysArgGluLysArgAsn 56
166 GAAAGGTCATGATGACATCATGAGAGACCTGACACAAATGACAGACA 215
|||||
57 GluAsnLeuLeuArgAspIleMetGluAspLeuAspThrAsnGlnAspAs 73
216 GCAGCTGAGCTTCGAGAGATTCATCATGCTGATGCGAGAGCTTAACCTGG 265
|||||
73 nGlnLeuSerPheGlnGluLysMetMetLeuMetGlyLysLeuIlePheA 90
266 CCTCCACGAGAAAGATGCAAGGGGTGACGAGGCGCTGGCCACACCACT 315
|||||
90 IAcYHisGlnLysLeuHisGlnAsnPro...ArgGlyHisAspHis 105
```

seq_name: p1r1:S68242

seq_documentation_block:

calgranulin B - mouse
N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory facto
C:Species: Mus musculus (house mouse)
C:Date: 09-Sep-1996 #sequence_revision 23-May-1997 #text_change 22-Jun-1999

C:Accession: S68242; S68272

R:Jagasse, E.; Weissman, I.L.

submitted to the EMBL Data Library, February 1992

A:Description: Mouse MRP8 and MRP14, two intracellular calcium-binding proteins assoc

A:Reference number: S68242

A:Accession: S68242

A:Molecule type: mRNA

A:Residues: 1-113 <LAG>

A:Cross-references: EMBL:M83219; NID:9199807; PIDN:AB07228.1; PID:9199808

R:Raftery, M.J.; Harrison, C.A.; Alewood, P.; Jones, A.; Geczy, C.L.

Biochem. J. 316, 285-293, 1996

A:Title: Isolation of the murine S100 protein MRP14 (14 kDa migration-inhibitory-fact

ding.

A:Reference number: S68272; MUID:96235204

A:Accession: S68272

A:Molecule type: protein

A:Residues: 2-10;95-109 <RAV>

A:Note: 107-His is identified as 3'-methylhistidine: the authors' source for the refe

ylhistidine

C:Genetics:

A:Gene: MRP14

C:Complex: heterodimer and higher complexes with calgranulin A

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation

F:2-113/Product: calgranulin B #status predicted <MAT>

F:11-45/Domain: calmodulin repeat homology <EF1>

F:55-87/Domain: calmodulin repeat homology <EF2>

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

F:80-91/Disulfide bonds: #status experimental

F:103,105,107/Binding site: zinc (His) #status predicted

F:107/Modified site: 3'-methylhistidine (His) #status experimental

alignment_scores:

Quality: 329.50 Length: 107
Ratio: 3.702 Gaps: 1
Percent Similarity: 83.178 Percent Identity: 59.813

alignment_block:

US-09-806-382a-2 x S68242 ..

Align seg 1/1 to: S68242 from: 1 to: 113

```
16 TCGCAGCTGAGCGACATGAGACATCATCAACACCTTCACCAATA 65
|||||
7 SerGlnMetGluArgSerIleThrIleIleAspThrPheHisGlnTy 23
66 CTCTGTGAGCTGGGGCCAGACACCTGACACCGAGGGGAATTCAG 115
|||||
23 rSerArgLysGlnGluHisProAspThrLeuSerLysLysGluPheArgG 40
116 AGCTGTGCGAAAGATCTGCAAAATTTTCTGAAGAGAGATTAAGAT 165
|||||
40 IuMetValGlnAlaGlnLeuAlaThrPheMetLysLysGluLysArgAsn 56
166 GAAAGGTCATGATGACATCATGAGAGACCTGACACAAATGACAGACA 215
|||||
57 GluAlaLeuIleAsnAspIleMetGluAspLeuAspThrAsnGlnAspAs 73
216 GCAGCTGAGCTTCGAGAGATTCATCATGCTGATGCGAGAGCTTAACCTGG 265
|||||
73 nGlnLeuSerPheGlnGluLysMetMetLeuMetAlaLysLeuIlePheA 90
266 CCTCCACGAGAAAGATGCAAGGGGTGAC...GAGGCGCTGGCCACAC 312
|||||
90 IAcYHisGlnLysLeuHisGlnAsnProArgGlyHisGlyHisSer 106
313 CATAAAGCAGGCGCTGGGGAG 333
|||||
107 HisGlyLysGlyCysGlyLys 113
```

seq_name: p1r2:J04712

```

seq.documentation.block:
S-100 calcium-binding protein A12 - human
M:Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; caltrophil protein
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 16-Jul-1996 #text_change 13-Aug-1999
C:Accession: J04712; J04717; J04891; S56113; S56114
R:Yamamura, T.; Hltoml, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsukada, Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping.
A:Reference number: J04712; MUID:96192053
A:Accession: J04712
A:Molecule type: mRNA
A:Residues: 1-92 <YAM>
A:Cross-references: DDBJ:D83657; NID:g1502284; PIDN:BAAL2030.1; PID:g1502285
R:Martl, T.; Ettmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequence
A:Reference number: J04717; MUID:96192069
A:Accession: J04717
A:Molecule type: Protein
A:Residues: 2-92 <MAP>
A:Experimental source: Onchocerca volvulus infecting human tissue
R:Ilid, E.C.; Troxler, H.; Buerjasser, D.M.; Kuster, T.; Markert, M.; Gulgnard, F.; Hunzli Biochem. Biophys. Res. Commun. 225, 146-150, 1996
A:Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP, C
A:Reference number: J04891; MUID:96332419
A:Accession: J04891
A:Molecule type: Protein
A:Residues: 2-92 <ILG>
R:Gulgnard, F.; Manel, J.; Markert, M.
Biochem. J. 309, 395-401, 1995
A:Title: Identification and characterization of a novel human neutrophil protein related
A:Reference number: S56113; MUID:95351965
A:Accession: S56113
A>Status: preliminary
A:Molecule type: protein
A:Residues: 'XX',4-14,'X',16-17,'XXXX' <GUII>
A:Experimental source: isoform 6a
A:Accession: S56114
A>Status: preliminary
A:Molecule type: protein
A:Residues: 2-21 <GUI2>
A:Experimental source: isoform 6b
C:Comment: This protein is released by activated neutrophils in the course of inflammatory
C:Genetics:
A:Gene: GDB:S100A12; p6; MRP6; CGRP; CAAF1
A:Cross-references: GDB:S218374
A:Map position: 1q21-1q21
C:Complex: monomer
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
P:2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAY>
P:6-39/Domain: calmodulin repeat homology <EFI>
F:49-81/Domain: calmodulin repeat homology <EF2>
F:86-90/Region: zinc binding #status predicted

alignment_scores:
Quality: 214.50 Length: 92
Ratio: 2.979 Gaps: 1
Percent Similarity: 78.261 Percent Identity: 46.739

alignment_block:
US-09-806-382A-2 x J04712 ..

Align seg 1/1 to: J04712 from: 1 to: 92

13 ATGTGCGAGTGGAGCGCAACATAGACGACCAACACTCCACCA 62
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetThrLysLeuGlnGlnIuhisLeuGluGlyIleValAsnIlepehisGI 17

63 ATACTCTGTGAAGCTGGGGCACCCAGACACCCCTGAACCGAGGGGGAATTCA 112

```

[illegible]

seq_name: p1r1:BCHUIB

seq_documentation_block:

S-100 protein beta chain
N:Alternate names: neutral S-100 calcium-binding protein beta
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 06-Jan-1995 #text_change 08-Dec-2000
C:Accession: A38364; A92972; A03076
R:Allore, R.J.; Friend, W.C.; O'Hanlon, D.; Neilson, K.M.; Bauman, R.; Dunn, R.J.; Marks, J. Biol. Chem. 265, 15537-15543, 1990
A:Title: Cloning and expression of the human S100beta gene.
A:Reference number: A38364; MUID:90368757
A:Accession: A38364
A:Molecule type: DNA
A:Residues: 1-92 <ALL>
A:Cross-references: GB:J05600; GB:M59486; NID:9337726; GB:M59487; NID:9337727; GB:M59488
R:Jensen, R.; Marshak, D.R.; Anderson, C.; Lukas, T.J.; Watterson, D.M.
J. Neurochem. 45, 700-705, 1985
A:Title: Characterization of human brain S100 protein fraction: amino acid sequence of S
A:Reference number: A92972; MUID:85291729
A:Accession: A92972
A:Molecule type: protein
A:Residues: 2-92 <GEN>
R:Baudier, J.; Glasser, N.; Haglid, K.; Gerard, D.
Biochim. Biophys. Acta 790, 164-173, 1984
A:Title: Purification, characterization and ion binding properties of human brain S100b
A:Reference number: A90653; MUID:85023393
A:Contents: annotation: metal ion-binding properties
C:Comment: This protein binds p53, tubulin and many other proteins at physiological conc
C:Comment: S-100 is an intracellular protein that binds calcium. It binds zinc more tigh
different affinities exist for both ions on each monomer. Physiological concentrations
nning sites.
C:Comment: This protein is expressed predominantly in brain tissue by astroglial cells.
C:Comment: The homodimer contains disulfide bonds, but the bond pattern has not been det
C:Genetics:
A:Gene: GDB:S100B
A:Cross-references: GDB:120360; OMIM:176990
A:Map position: 21q22.3-21q22.3
A:Introns: 46/3
A>Note: the first intron occurs before the initiator codon
C:Complex: homodimer; heterodimer with S-100 protein alpha chain (see PIR:BCHUIA)
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; brain; calcium binding; EF hand; heterodimer; homodimer;
F:2-92/Product: S-100 protein beta chain #status experimental <MAT>
F:6-40/Domain: calmodulin repeat homology <EPF2>
F:49-81/Domain: calmodulin repeat homology <EPF2>
F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
F:19,22,24,27,32/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
F:62,64,66,68,73/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted

alignment_scores:

Quality:	177.50	Length:	88
Ratio:	2.536	Gaps:	1
Percent Similarity:	79.545	Percent Identity:	39.773

alignment_block:

US-09-806-382A-2 x BCHUIB ..

Align seg 1/1 to: BCHUIB from: 1 to: 92

```
13 ATGTCTGACGTGAGACCAATAGACCATCATGACACCTTCACCA 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetSerGluLeuIleuLysAlaMetValAlaLeuIleAspValPheHisGcl 17
63 ATATCTGTGACAGCTGGGACACCAACACCTGAACACGAGGGAATTC 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 ntyrSerGlyArgGluGlyAspLysHisLysLysLysSerGluLeuL 34
113 AAGAGCTGGGAGGAAGAATCTCAAAATTTCTCAAGAGGAGATTAAG 162
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 yseIleuIleAsnGluLeuSerHisPheLeu...GluIleuLys 49
```

163 AATGAAAGCTCATAGACACATCATGACGACCTGGACACAATGACAGA 212
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
50 GUGInGluValValAspLysValMetGluThrLeuAspHisnspLys 66
213 CAAGCAGCTGACCTTCGAGAGATTTCATCATGCTGATGGCAGACTTA 262
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
66 pglGluGlyAspPheGlnIlePheMetAlaPheValIleMetValThr 83
263 GGGCTTCGCCAGAG 276
||| |||||
83 hralAcYsHisGlu 87

seq_name: p1r1:BCBOIB

seq_documentation_block:

S-100 protein beta chain - bovine
N:Alternate names: neurolcalcin delta-binding protein S100-beta
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-May-1979 #sequence_revision 14-Nov-1983 #text_change 24-Nov-1999
C:Accession: A91254; B91110; A90075; S54348; A03077
R:Isobe, T.; Okuyama, T.
Eur. J. Biochem. 89, 379-388, 1978
A:Title: The amino-acid sequence of S-100 protein (PAP-I-b protein) and its relation
A:Reference number: A91254; MUID:79045265
A:Accession: A91254
A:Molecule type: protein
A:Residues: 'ESGL', 5-91 <ISO>
A:Experimental source: brain
A>Note: this sequence has since been revised in reference A91110
R:Isobe, T.; Okuyama, T.
Eur. J. Biochem. 116, 79-86, 1981
A:Title: The amino-acid sequence of the alpha subunit in bovine brain S-100 a protein
A:Reference number: A91110; MUID:81236562
A:Accession: B91110
A:Molecule type: protein
A:Residues: 1-91 <IS2>
R:Baudier, J.; Gerard, D.
Biochemistry 22, 3360-3369, 1983
A:Title: Ions binding to S100 proteins: structural changes induced by calcium and zin
A:Reference number: A90471; MUID:84000339
A:Contents: annotation: metal ion-binding properties
R:Marshak, D.R.; Umekawa, H.; Watterson, D.M.; Hidak, H.
Arch. Biochem. Biophys. 240, 777-780, 1985
A:Title: Structural characterization of the calcium binding protein S100 from adipose
A:Reference number: A90075; MUID:85278169
A:Accession: A90075
A:Molecule type: protein
A:Residues: 1-91 <MAR>
A:Experimental source: adipose tissue
R:Okazaki, K.; Obata, N.H.; Inoue, S.; Hidak, H.
Biochem. J. 306, 551-555, 1995
A:Title: S100-beta is a target protein of neurolcalcin delta, an abundant isoform in g
A:Reference number: S54343; MUID:95194333
A:Accession: S54348
A:Molecule type: protein
A:Residues: 56-61, 'N', 63-79, 'V' <OKA>
C:Comment: The S-100 protein is composed of two related polypeptide chains, alpha and
brain proteins. S-100 is also found in a variety of other tissues.
C:Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc
es with different affinities exist for both ions on each monomer. Physiological conce
cium-binding sites.
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; brain; calcium binding; EF hand; zinc
F:5-39/Domain: calmodulin repeat homology <EPF1>
F:48-80/Domain: calmodulin repeat homology <EPF2>
F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental
F:18,21,23,26,31/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
F:61,63,65,67,72/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted

alignment_scores:

Quality:	176.50	Length:	87
Ratio: <td>2.558</td> <td>Gaps:<td>1</td></td>	2.558	Gaps: <td>1</td>	1

S-100 protein alpha chain - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 14-Nov-1983 #sequence_revision 06-Feb-1995 #text_change 24-Nov-1999
 C:Accession: A24156; A91110; S54346; A03078
 R:Kuwano, R.; Maeda, T.; Usui, H.; Araki, K.; Yamakuni, T.; Ohshima, Y.; Kurihara, T.;
 FEBS Lett. 202, 97-101, 1986
 A>Title: Molecular cloning of cDNA of S100alpha subunit mRNA.
 A:Reference number: A24156; MUID:86248083
 A:Accession: A24156
 A:Molecule type: mRNA
 A:Residues: 1-94 <KUM>
 R:Isobe, T.; Okuyama, T.
 Eur. J. Biochem. 116, 79-86, 1981
 A>Title: The amino acid sequence of the alpha subunit in bovine brain S-100 a protein.
 A:Reference number: A91110; MUID:81236562
 A:Accession: A91110
 A:Molecule type: Protein
 A:Residues: 2-64, 'D', 66-94 <ISO>
 R:Baudier, J.; Gerard, D.
 Biochemistry 22, 3360-3369, 1983
 A>Title: Ions binding to S100 proteins: structural changes induced by calcium and zinc c
 A:Reference number: A90471; MUID:84000339
 A:Contents: annotation; metal ion-binding properties
 R:Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
 Biochem. J. 306, 551-555, 1995
 A>Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia
 A:Reference number: S54343; MUID:95194333
 A:Accession: S54346
 A:Molecule type: Protein
 A:Residues: 24-33 <OKA>
 C:Comment: The S-100 protein is composed of two related polypeptide chains, alpha and be
 brain proteins. S-100 is also found in a variety of other tissues.
 C:Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc ve
 es, with different affinities, exist for both ions on each monomer. Physiological concen
 alcium-binding sites.
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: blocked amino end; brain; calcium binding; EF hand; zinc
 F:2-94/Product: S-100 protein alpha chain #status predicted <MAT>
 F:7-41/Domain: calmodulin repeat homology <EF1>
 F:50-82/Domain: calmodulin repeat homology <EF2>
 F:20/23, 25, 28, 33/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
 F:63, 65, 67, 69, 74/Binding site: calcium (Asp, Asn, Asp, Glu, Glu) #status predicted

alignment_scores:
 Quality: 161.50 Length: 84
 Ratio: 2.563 Gaps: 1
 Percent Similarity: 75.000 Percent Identity: 39.286

alignment_block:
 US-09-806-382a-2 x BCBO1A ..

Align seg 1/1 to: BCBO1A from: 1 to: 94

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16 TCGCAGCTGGAAAGCGACATGAGACCATCATCAACACCTTCCACCATA 65
|||||
3 SerGluLeuGluThrAlaMetGluThrLeuIleAsnValPheHisAlaH1 19
66 CTCTGTGAAGCTGGGGCACCAGACACCTGTGACACGGGGAATTCAG 115
|||||
19 SerGluLysGluGluLysPlySTyLysLeuSerLysLysGluLeuLysG 36
116 AGCTGTGGGAAAAGATCTGCAAAATTTCTCAAGAGAGAGAAATAGAT 165
|||||
36 IuLeuLeuGlnThrGluLeuSerGlyPheLeuAspAlaGln...LysAsp 51
166 GAAAGGTCATAGAACACATCATGAGAGACCTGACACAAATGACAGCAA 215
|||||
52 AlaAspAlaValAspLysValMetLysGluLeuAspGluAsnGlyLysPgl 68
216 GCAGCTGAGCTTCGAGAGTTCATCATGCTGATGCGGAGCTAACCTGG 265
|||||

```

68 ygluValAspPheGlnGluTyValValLeuValAlaAlaLeuThrValA 85
 266 CC 267
 85 la 85

seq_name: pIR1: BCHUIA

seq documentation_block:
 S-100 protein alpha chain - human
 N:Alternate names: S-100 calcium-binding protein A1 (S100A1)
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1993 #sequence_revision 23-May-1997 #text_change 22-Jun-1999
 C:Accession: A44470; S16740
 R:Engelkamp, D.; Schafer, B.W.; Erne, P.; Heizmann, C.W.
 Biochemistry 31, 10258-10264, 1992
 A>Title: S100 alpha, CAPL, and CACY: molecular cloning and expression analysis of thr
 A:Reference number: A44470; MUID:93041710
 A:Accession: A44470
 A:Molecule type: mRNA
 A:Residues: 1-94 <ENG>
 A:Cross-references: EMBL:X58079; NID:g36175; PIDN:CAA41107.1; PID:g36176
 A:Experimental source: heart
 A:Note: sequence extracted from NCBI backbone (NCBIP:116494)
 C:Comment: This protein binds p53, tubulin and many other proteins at physiological c
 different affinities exist for both ions on each monomer. Physiological concentratio
 nding sites.
 C:Comment: Although predominant among the water-soluble brain proteins, S-100 is also
 C:Genetics:
 A:Gene: GDB:S100A1; S100A
 A:Cross-references: GDB:126839; OMIM:176940
 A:Map position: 1q21-1q21
 C:Complex: homodimer; heterodimer with S-100 protein beta chain (see PIR:BCHUIB)
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: brain; calcium binding; EF hand; heterodimer; homodimer; zinc
 F:7-41/Domain: calmodulin repeat homology <EF1>
 F:50-82/Domain: calmodulin repeat homology <EF2>

alignment_scores:
 Quality: 160.50 Length: 84
 Ratio: 2.548 Gaps: 1
 Percent Similarity: 75.000 Percent Identity: 39.286

alignment_block:
 US-09-806-382a-2 x BCHUIA ..

Align seg 1/1 to: BCHUIA from: 1 to: 94

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16 TCGCAGCTGGAAAGCGACATGAGACCATCATCAACACCTTCCACCATA 65
|||||
3 SerGluLeuGluThrAlaMetGluThrLeuIleAsnValPheHisAlaH1 19
66 CTCTGTGAAGCTGGGGCACCAGACACCTGTGACACGGGGAATTCAG 115
|||||
19 SerGluLysGluGluLysPlySTyLysLeuSerLysLysGluLeuLysG 36
116 AGCTGTGGGAAAAGATCTGCAAAATTTCTCAAGAGAGAGAAATAGAT 165
|||||
36 IuLeuLeuGlnThrGluLeuSerGlyPheLeuAspAlaGln...LysAsp 51
166 GAAAGGTCATAGAACACATCATGAGAGACCTGACACAAATGACAGCAA 215
|||||
52 ValAspAlaValAspLysValMetLysGluLeuAspGluAsnGlyLysPgl 68
216 GCAGCTGAGCTTCGAGAGTTCATCATGCTGATGCGGAGCTAACCTGG 265
|||||
68 ygluValAspPheGlnGluTyValValLeuValAlaAlaLeuThrValA 85
266 CC 267
85 la 85

```

seq_name: p1r2:A41988

seq_documentation_block:

S-100 calcium-binding protein A2 - human
N:Alternate names: calcium-binding protein Can19; S-100 calcium-binding protein L
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Aug-1997
C:Accession: A41988
R:Lee, S.W.; Tomasetto, C.; Swisshelm, K.; Keyomarsi, K.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 2504-2508, 1992
A:Title: Down-regulation of a member of the S100 gene family in mammary carcinoma cells
A:Reference number: A41988; MUID:92196147
A:Accession: A41988
A:Molecule type: mRNA
A:Residues: 1-98 <LEP>
A:Cross-references: GB:M87068; NID:q179896
A:Experimental source: mammary carcinoma cells
A>Note: sequence extracted from NCBI backbone (NCBIN:88561, NCBI:P:88562)
C:Genetics:
A:Gene: GDB:S100A2; CAN19; S100L
A:Cross-references: GDB:211118; OMIM:176993
A:Map position: 1q21-1q21
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:8-42/Domain: calmodulin repeat homology <EFL>
F:51-83/Domain: calmodulin repeat homology <EF2>

alignment_scores:

Quality:	156.50	Length:	87
Ratio:	2.371	Gaps:	2
Percent Similarity:	75.862	Percent Identity:	36.782

alignment_block:

US-09-806-382a-2 x A41988 ..

Align seg 1/1 to: A41988 from: 1 to: 98

```
1 ATGACCTGCAAAATGTCGACGTGGAACGACACATAGAGACCATCA 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 MetMetCys.....SerSerLeuGluGlnAlaLeuAlaValLeuAla 15
51 CACCTTCCACCAATCTGTGTGAGAGCTGGGGACCCAGACACCCCTG 100
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
15 rhrhrhnhslstysrSerCysGlnGlnIuGlnAspIysPheIysLeu 32
101 AGGGGGAATTCGAAGAGCTGGTGGCAAAAGATGCAAAATTTTCTCA 150
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
32 ysgIuIuMetIysGluLeuLeuIuIysGluLeuProSerPheVal... 47
151 AAGGAGATATAGATGAAAAAGTCAATAGAACACATCATGAGAGCTG 200
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48 GluGluIuIuValAspIuGlnIuGlnLeuIysIysLeuMetCylAsnLeu 64
201 CACAAATGCAAGACAGACAGCTGAGTTGAGAGATTCAATCATCTGATG 250
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
64 pgluAsnSerAspGlnGlnIuValAspPheGlnGlnIuTyAlaValAl 81
251 CGAGGCTAAC 261
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
81 lAluLeuIleThr 84
```

seq_name: p1r2:A45135

seq_documentation_block:

Profilaggrin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999
C:Accession: A45135
J:Presland, R.B.; Haydock, P.V.; Fleckman, P.; Mirunskis, I.; Dale, B.A.
J. Biol. Chem. 267, 23772-23781, 1992
A:Title: Characterization of the human epidermal profilaggrin gene. Genomic organization

A:Reference number: A45135; MUID:93054736

A:Accession: A45135

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-591 <PRE>

A:Cross-references: GB:L01089; GB:M90967; NID:q190408; PIDN:AAA60177.1; PID:9553621

A>Note: sequence extracted from NCBI backbone (NCBIP:118773)

C:Genetics:

A:Gene: GDB:FIG

A:Cross-references: GDB:119912; OMIM:135940

A:Map position: 1q21-1q21

C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology

C:Keywords: EF hand; epidermis; polymorphism; tandem repeat

F:49-81/Domain: calmodulin repeat homology <EF2>

alignment_scores:

Quality:	154.00	Length:	103
Ratio:	2.081	Gaps:	2
Percent Similarity:	71.845	Percent Identity:	35.922

alignment_block:

US-09-806-382a-2 x A45135 ..

Align seg 1/1 to: A45135 from: 1 to: 591

```
13 ATGTGCGACGTGGAACGACACATAGAGACCATCATCAACCTCCACA 62
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 MetSerThrLeuLeuGlnAsnIlePheAlaIleIleAsnLeuPheIysG 17
63 ATACTCTGTGAGAGCTGGGGACCCAGACACCCCTGAACCAAGGGGA 112
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
17 nIySerIysAspIysAsnThrAspThrLeuSerIysGluLeuIu 34
113 AAGAGCTGTCGCAAAAGATCTGCAAAATTTCTCAAGAGAGATTAAG 162
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
34 ysgIuLeuLeuGlnIuIysGluPheArgIuIleuIuIysAsnProAsp... 49
163 AATGAAGGTCATAGAACACATCATGAGAGACCTGGACACAAATGCA 212
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
50 AspProAspMetValAspAlaPheMetIAspIleuAspIleAsnIys 66
213 CAAGCAGCTGAGCTTGAAGAGATTCATAGCTGATGCGCAGGCTAAC 262
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 nIyIysIleAspPheThrGluPheLeuMetValPheIysLeuAlaG 83
263 GAGCCTCCACGAGAGATGAC...GAGGGTGACAGAGGCGCTGGCCAC 309
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
83 lnaIaTyTyGluSerThrArgIyGlnAsnLeuProIleSerGlyHis 99
310 CACCATTAAG 318
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
100 LysHisArg 102
```


OM of: US-09-806-382A-2 to: SwissProt_40:* out_format : pfs
Date: Sep 9, 2002 3:22 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODE=frame-n2p,model -DEV=xlp
-O=/cgn2_1/USPTO.spool/US09806382/runat.09092002_143849_15565/app-query.fasta.1.752
-DB=SwissProt_40 -OPMT=fastan -SUFFIX=exp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -VGAPOP=10.000 -VGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blotsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09806382.ecgnl.1.62 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-806-382A-2
Query length: 345
Database: SwissProt_40:*
Database sequences: 105224
Database length: 38719550
Search time (sec): 32.310000

score_list:

Sequence	Strid	Orig	ZScore	Escore	Len	Documentation
SwissProt_40:S109_BOVIN	386.50	630.20	1.7e-27	122	P28783 bos taurus (bovine).	
SwissProt_40:S109_RAT	353.50	577.33	1.6e-24	112	P50116 rattus norvegicus (rat).	
SwissProt_40:S109_MOUSE	329.50	538.39	2.4e-22	112	P31725 mus musculus (mouse).	
SwissProt_40:S109_RABIT	328.00	535.55	3.3e-22	118	P50117 oryctolagus cuniculus	
SwissProt_40:M126_CHICK	216.00	353.77	4.4e-12	119	P28318 gallus gallus (chicken)	
SwissProt_40:S112_PIG	213.50	351.81	7.4e-12	91	P80310 sus scrofa (pig).	
SwissProt_40:S112_HUMAN	209.50	340.32	1.7e-11	91	P80511 homo sapiens (human).	
SwissProt_40:S112_BOVIN	206.50	334.45	3.2e-11	91	P79105 bos taurus (bovine).	
SwissProt_40:S112_RABIT	181.50	300.80	5.8e-09	81	O77791 oryctolagus cuniculus	
SwissProt_40:S112_BOVIN	176.50	291.78	1.6e-08	91	P02638 bos taurus (bovine).	
SwissProt_40:S108_HUMAN	172.50	285.29	3.7e-08	91	P04271 homo sapiens (human).	
SwissProt_40:S108_MOUSE	171.50	283.67	4.6e-08	91	P50114 mus musculus (mouse).	
SwissProt_40:S108_RAT	168.50	278.80	8.6e-08	91	P04631 rattus norvegicus (rat).	
SwissProt_40:S108_HUMAN	165.50	273.60	1.6e-07	95	P25815 homo sapiens (human).	
SwissProt_40:S10A_RAT	162.50	268.90	3.0e-07	93	P35467 rattus norvegicus (rat).	
SwissProt_40:S10A_BOVIN	161.50	267.27	3.7e-07	93	P02639 bos taurus (bovine).	
SwissProt_40:S10A_HUMAN	160.50	265.65	4.5e-07	93	P23287 homo sapiens (human).	
SwissProt_40:S102_HUMAN	154.50	255.59	1.6e-06	97	P29034 homo sapiens (human).	
SwissProt_40:S102_BOVIN	153.50	253.96	2.0e-06	97	P10462 bos taurus (bovine).	
SwissProt_40:S111_RABIT	153.50	253.57	2.0e-06	102	P24480 oryctolagus cuniculus	
SwissProt_40:S10A_MOUSE	152.50	252.67	2.4e-06	93	P56565 mus musculus (mouse).	
SwissProt_40:S104_HUMAN	150.50	248.78	3.6e-06	101	P26447 homo sapiens (human).	
SwissProt_40:S111_HUMAN	149.50	246.85	4.5e-06	105	P31949 homo sapiens (human).	
SwissProt_40:S104_MOUSE	149.00	246.35	5.0e-06	101	P07091 mus musculus (mouse).	
SwissProt_40:S104_BOVIN	147.00	243.18	7.5e-06	100	P35466 bos taurus (bovine).	
SwissProt_40:S108_MOUSE	146.50	243.37	8.4e-06	88	P27005 mus musculus (mouse).	
SwissProt_40:S101_ICPUP	144.50	239.05	1.3e-05	92	P091061 ictalurus punctatus (cat)	
SwissProt_40:S108_RAT	143.50	238.50	1.6e-05	88	P50115 rattus norvegicus (rat).	
SwissProt_40:S106_CHICK	143.50	238.15	1.6e-05	92	P08953 gallus gallus (chicken)	
SwissProt_40:S105_MOUSE	140.50	233.20	2.9e-05	93	P08945 mus musculus (mouse).	
SwissProt_40:S111_MOUSE	140.50	232.79	2.9e-05	98	P50543 mus musculus (mouse).	
SwissProt_40:S104_RAT	140.00	231.75	3.2e-05	101	P05942 rattus norvegicus (rat).	
SwissProt_40:S107_BOVIN	140.00	231.75	3.2e-05	101	P028650 bos taurus (bovine).	
SwissProt_40:S105_HUMAN	139.00	229.46	4.0e-05	110	P33763 homo sapiens (human).	
SwissProt_40:S113_HUMAN	138.00	228.74	4.9e-05	98	P09384 homo sapiens (human).	
SwissProt_40:S106_RABIT	137.50	228.59	5.4e-05	90	P30801 oryctolagus cuniculus	
SwissProt_40:S106_HORSE	137.00	227.61	6.0e-05	92	O77691 equus caballus (horse)	
SwissProt_40:S111_CHICK	135.50	224.44	8.3e-05	101	P24479 gallus gallus (chicken)	
SwissProt_40:S106_RAT	135.00	224.53	9.2e-05	90	P05964 rattus norvegicus (rat).	
SwissProt_40:S106_MOUSE	134.00	223.00	0.0001	89	P14069 mus musculus (mouse).	

SwissProt_40:S106_HUMAN	134.00	222.91	0.0001	90	P06703 homo sapiens (human)
SwissProt_40:S108_HUMAN	133.50	221.84	0.0001	93	P05109 homo sapiens (human)
SwissProt_40:S110_CHICK	128.00	212.67	0.0004	96	P27003 gallus gallus (chicken)
SwissProt_40:S110_MOUSE	128.00	212.67	0.0004	96	P08207 mus musculus (mouse)

seq_name: SwissProt_40:S109_BOVIN

seq_documentation_block:
ID S109_BOVIN STANDARD; PRT; 122 AA.

AC P28783;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calgranulin B (Neutrophil cytosolic 23 kDa protein) (P23) (BEE22)
DE (Fragment).
GN S100A9.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX MEDLINE=93280230; PubMed=8505358;
RA Tang T.-K., Hong T.-M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-J.,
Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.-C.,
Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;
RT "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
RT antibody W2 specifically reacts with condensed nuclei of
RT differentiated superficial cells."
RL J. Cell Sci. 104:237-247(1993).
RN [2]
RP SEQUENCE OF 4-56.
RC TISSUE=Neutrophils;
RX MEDLINE=92304974; PubMed=1610833;
RA Dianoux A.-C., Stasia M.-J., Garin J., Gagnon J., Vignais P.V.;
RT "The 23 kDoladon protein, a substrate of protein kinase C, in
RT Biochemistry 31:5898-5905(1992).
RL - SUBUNIT. DISULFIDE LINKED HETERODIMER OF A 7/11 kDa AND A 22/23
CC KDA SUBUNITS.
CC - SUBCELLULAR LOCATION. CYTOPLASMIC; LOOSELY ASSOCIATED TO THE
CC CYTOSKELETON.
CC - TISSUE SPECIFICITY: FOUND ESSENTIALLY IN PHAGOCYTTIC CELLS.
CC - PTM: PHOSPHORYLATED BY PROTEIN KINASE C.
CC - MISCELLANEOUS: CONTAINS TWO CA(2+)-BINDING DOMAINS PER PROTEIN.
CC - SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC - SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
DR HSP: P02638; IMHO.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_CaBP.
DR Pfam: PF00036; efhand; 1.
DR Pfam: PF01023; S100; 1.
DR PROSITE: PS00018; EF_HAND; PARTIAL.
DR PROSITE: PS00303; S100_CaBP; 1.
KW Calcium-binding; Phosphorylation.
FT NON_TER 1 1
FT CA_BIND 19 32 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 63 74 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
SQ SEQUENCE 122 AA; 13673 MW; F3CA8C4806BCCD CRC64;

alignment_scores:

Quality:	386.50	Length:	109
Ratio:	4.068	Gaps:	1
Percent Similarity:	87.156	Percent Identity:	70.642

alignment_block:

US-09-806-382A-2	x	S109_BOVIN	..
Align seg 1/1	to:	S109_BOVIN	from: 1 to: 122

```

13  ANTCGACAGCTGGAGCAACATAGACCATCATCAACACCTTCACCA 62
14  |||||||:||||:|||||||||||||||||  |||||||
15  MetSerGlnMetGlnSerSerIleGluThrIleIleAsnIlePheHisGly 17
16  63  ATACTCTGTGAAGCTGGGACACCCAGACACCTGAAACCAAGGGGAATTCA 112
17  |||||||:|||||:|||||  |||||||
18  nTyrSerValArgLeuGluGlyHisIleTyrAspThrLeuIleGlnTyrGluPheL 34
19  113  AAGAGCTGTGGCAAGAAATCTCCAAATTTCTCAAGAAGGAATTAAG 162
20  |||||||:|||||:|||||  |||||||
21  ySGLInLeuValGlnTyrGluLeuProAspPheLeuTyrSlySglnTyrLys 50
22  163  AATGAAAGGTCATAGACACATCATGAGGAGCACTGAGACAAATTCAGA 212
23  |||||||  :|||||:|||||:|||||  |||||||
24  51  AaGlnAlaIleAlaIleAsnGluIleMetGluAspLeuAspThrAsnValAs 67
25  213  CAAAGCAGCTGAGCTTCGAGAGTTCATCATGCTGATGCGAGGCTTAACCT 262
26  |||||||:|||||:|||||  |||||||
27  67  pTyrSglnLeuSerPheGluGluPheIleMetLeuValAlaArgLeuThrTy 84
28  263  GGGCCCTCCAGAGAGATGACAGAG...GGTACAGAGGGCCCTGGCCAC 309
29  |||||||:|||||:|||||  |||||||
30  84  aAlaSerHisGlnGluMetHisAsnThrAlaProProGlyGlnGlyHis 100
31  310  CACCATAGCCAGAGGCTCGGGAGGAGGC 336
32  |||||||  |||||||  |||||||
33  101  ArgHisGlyProGlyTyrGlyTyrGlySgly 109

```

seq_name: SwissProt_40:S109_RAT

seq_documentation_block: PRT: 112 AA.

```

ID  S109_RAT  STANDARD;  PRT: 112 AA.
AC  P50116;
DT  01-OCT-1996 (Rel. 34, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Calgranulin B (Migration inhibitory factor-related protein 14)
DE  (MRP-14) (P14).
GN  S100A9 OR MRP14.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=LEWIS/N; TISSUE=peritoneal cavity;
RX  MEDLINE=93343942; PubMed=8343166;
RA  Imamiuchi T., Uchida I., Wahl S.M., McCartney-Francis N.;
RT  "Expression and cloning of migration inhibitory factor-related
RL  protein (MRP)8 and MRP14 in arthritis-susceptible rats.";
RL  Biochem. Biophys. Res. Commun. 194:819-825(1993).
RN  [2]
RP  SEQUENCE OF 1-56; 61-64 AND 71-112, ACETYLTATION, AND METHYLATION.
RC  TISSUE=Spleen;
RX  MEDLINE=98249881; PubMed=9570842;
RA  Raftery M.J., Geecy C.L.;
RT  "Identification of posttranslational modifications and cDNA sequencing
RT  errors in the rat S100 proteins MRP8 and 14 using electrospray
RT  ionization mass spectrometry.";
RL  Anal. Biochem. 258:285-292(1998).
CC  -1- MASS SPECTROMETRY: MW=13069; MW_ERR=2; METHOD=Electrospray.
CC  -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC  -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; L18948; AAA18214.1; -.

```

```

DR  HSSP; P02638; 1MHO.
DR  InterPro: IPR002048; EF-hand.
DR  InterPro: IPR001751; S100_Cabp.
DR  Pfam; PF01023; S_100; 1.
DR  SMART; SM00054; EFh; 1.
DR  PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR  PROSITE; PS00303; S100_CABP; 1.
KW  Calcium-binding; Acetylation; Methylation.
FT  INIT_MET 0
FT  MOD_RES 1 0
FT  MOD_RES 1 106 ACETYLTATION.
FT  CA_BIND 23 36 METHYLATION.
FT  CA_BIND 67 78 EF_HAND 1 (LOW AFFINITY) (POTENTIAL).
FT  CONFLICT 105 105 EF_HAND 2 (HIGH AFFINITY) (POTENTIAL).
SQ  SEQUENCE 112 AA; 13014 MW; 381EBB291175D068 CRC64;

```

alignment_scores: Quality: 353.50 Length: 107

Percent Similarity: 85.981 Ratio: 3.842 Gaps: 1

Percent Identity: 64.486

US-09-806-382a-2 x S109_RAT

Align seg 1/1 to: S109_RAT from: 1 to: 112

alignment_block:

```

16  TCGCAGCTGGAGCAACATAGACCATCATCAACACCTTCACCAATA 65
17  |||||||:|||||:|||||  |||||||
18  6  SerGlnLeuArgSerSerIleGluThrIleIleAsnValPheHisGlnTy 22
19  66  CTCTGTAAGCTGGGACACCCAGACACCTGAGACCAAGGGGAATTCAAG 115
20  |||||||  |||||||:|||||:|||||  |||||||
21  22  tSerArgLysTyrGlyHisProAspThrLeuAsnLysAlaGluPheLysG 39
22  116  AGCTGTGGCAAGAAATCTCCAAATTTCTCAAGAAGGAATTAAGAAAT 165
23  |||||||:|||||:|||||  |||||||:|||||:|||||
24  39  LuMetValAsnLysAspLeuProAspPheLeuTyrSlySglnTyrLys 55
25  166  GAAAGGTCATAGACACATCATGAGGAGCCTGAGACACAAATGCACAGAA 215
26  |||||||:|||||:|||||  |||||||
27  56  GluAsnLeuLeuArgAspIleMetGluAspLeuAspThrAsnValAsn 72
28  216  GCAGCTGAGCTTCGAGAGTTCATCATGCTGATGCGAGGCTTAACCTGG 265
29  |||||||:|||||:|||||  |||||||
30  72  nGlnLeuSerPheGluGluLysMetLeuMetGlyLysLeuIlePheAs 89
31  266  CTTCCAGCAGAGAAATGACAGAGGAGGAGGCGCTGGCCACACCAAT 315
32  |||||||:|||||:|||||  |||||||
33  89  LacysHisGlnTyrLeuHisGluAsnAsnPro...ArgGlyHisAspHis 104
34  316  AAGCCAGGCTCGGGAGGAGGC 336
35  |||||||  |||||||  |||||||
36  105  SerHisGlyLysGlyCysGly 111

```

seq_name: SwissProt_40:S109_MOUSE

seq_documentation_block:

```

ID  S109_MOUSE  STANDARD;  PRT: 112 AA.
AC  P31725;
DT  01-JUL-1993 (Rel. 26, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  01-MAR-2002 (Rel. 41, Last annotation update)
DE  Calgranulin B (Migration inhibitory factor-related protein 14)
DE  (MRP-14) (P14) (Leukocyte LI complex heavy chain).
GN  S100A9 OR CAGB OR MRP14.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/C;

```

```

RX MEDLINE=92223366; PubMed=1373330;
RA Lagasse E., Weissman I.L.;
RT "Mouse MRP8 and MRP14, two intracellular calcium-binding proteins
RL associated with the development of the myeloid lineage.";
RN Blood 79:1907-1915(1992).
RC [2]
RD SEQUENCE FROM N.A.
RE STRAIN=129/SVJ;
RA Nacker W.K.F., Lekstrom-Himes J.A., Sorg C., Manitz M.;
RT "Molecular analysis of the mouse S100A9 gene and evidence that the
RL myeloid specific transcription factor C/EBPepsilon is not required for
RT the regulation of the S100A9/A8 gene expression in neutrophils.";
RL J. Cell. Biochem. 80:606-616(2001).
RN [3]
RP SEQUENCE OF 1-9; 75-92 AND 94-108.
RX MEDLINE=96235204; PubMed=8645219;
RA Rattery M.J., Harrison C.A., Alewood P., Jones A., Geczy C.L.;
RT "Isolation of the murine S100 protein MRP14 (14 kDa
RL migration-inhibitory-factor-related protein) from activated spleen
RT cells: characterization of post-translational modifications and zinc
RT binding.";
RL Biochem. J. 316:285-293(1996).
CC -1- MASS SPECTROMETRY: MW=12972; MW_ERR=2; METHOD=Electrospray.
CC -1- MISCELLANEOUS: HAS BEEN SHOWN TO BIND CALCIUM.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M83319; AAB07228.1; -.
DR EMBL; AJ250496; CAC14292.1; -.
DR HSSP; P02638; IMHO
DR MGD; MGI:1338947; S100a9.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_CaBP.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CaBP; 1.
KW Calcium-binding; Acetylation; Methylation.
FT INT_MET 0
FT CA_BIND 23 36 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 67 78 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
FT DISULFD 79 90
FT MOD_RES 1 1 ACETYLATION.
FT MOD_RES 106 106 METHYLATION.
SQ SEQUENCE 112 AA; 12918 MW; ADF810BC175AEC80 CRC64;

```

alignment_scores:

Quality: 329.50 Length: 107
Ratio: 3.702 Gaps: 1
Percent Similarity: 83.178 Percent Identity: 59.813

alignment_block:

US-09-806-382A-2 x S109_MOUSE ..

Align seg 1/1 to: S109_MOUSE from: 1 to: 112

```

16 TCGCAGCTGGAAGCAACATAGACATCATACACCTTCACCAATA 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
6 SerGlnMetGluArgSerIleThrIleIleLeuAspThrPheHisGlnTyr 22
66 CTCTGTGAAGCTGGGGCAGCCAGACACCTGGAACAGGGGGAATTCAAG 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
22 rSerArgTyrGlnGluGlnHisProAspThrIleuSerTyrGlnPheArg 39

```

```

116 AGCTGTGCGAAAGATGTCGAAATTTTCAGAGAGAGAAATAAAT 165
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
39 lMetValGluAlaGlnIleuAlaThrPheMetLysLysGluLysArgAsn 55
166 GAAAGGTGATGAGAACACATCATGAGAGACCTGGACCAATATGACAGCAA 215
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
56 GluAlaLeuIleAsnAspIleMetGluAspLeuAspPheHisGlnAspAs 72
216 CGAGCTGAGCTTCGAGAGATTCATCATGCTGATGGCAGAGCTAACTGGG 265
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
72 nGlnIleuSerPheGlnGluGlnCysMetMetLeuMetAlaLysLeuIlePhe 89
266 CTTCCGACGAGAGATGACGAGGGTGAC...GAGGGCCTCGCCACACAC 312
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
89 lAcYrSHSLysLysLysIleuHisGlnIleAsnProArgLysHisSer 105
313 CATAGCGCAGCGCTCGGGGAG 333
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
106 HisGlyLysGlyCysGlyLys 112

```

seq_name: SwissProt_40:S109_RABIT

seq_documentation_block:

ID S109_RABIT STANDARD; PRT; 118 AA.

AC P50117;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calgranulin B (Migration inhibitory factor-related protein 14)

GN (MRP-14) (Fragment).

DE S100A9 OR MRP-14.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

ON NCBI_TaxID=9986;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN-NEW ZEALAND WHITE; TISSUE-Neutrophils;

RX MEDLINE=96355278; PubMed=8702688;

RA Yang Z., de Veer M.J., Gardiner E.E., Devanish R.J., Handley C.J.,

RA Underwood J.R., Robinson H.C.;

RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-

RL calgranulin C when incubated with inorganic [35S]sulfate.";

RL J. Biol. Chem. 271:19802-19809(1996).

RN [2]

RP SEQUENCE OF 45-82 FROM N.A.

RC STRAIN-NEW ZEALAND WHITE;

RX MEDLINE=94198229; PubMed=8148323;

RA Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;

RT "Dynamic changes in mRNA expression of neutrophils during the course

RL of acute inflammation in rabbits.";

RL Int. Immunol. 6:149-156(1994).

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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CC -----

DR EMBL; AF091849; AAC61771.1; -.

DR EMBL; D17404; BAA04227.1; -.

DR HSSP; P02638; IMHO.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001751; S100_CaBP.

DR Pfam; PF00036; efhand; 1.

DR Pfam; PF01023; S_100; 1.

DR PROSITE; PS00018; EF_HAND; 1.

DR PROSITE; PS00303; S100_CaBP; 1.

KW Calcium-binding; Repeat.

```

FT NON_TER 1 1
FT CA_BIND 9 22 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 53 64 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
FT DOMAIN 103 118 2 X 8 AA TANDEM REPEATS OF G-H-G-H-
FT REPEAT 103 110 1.
FT REPEAT 111 118 2.
SO SEQUENCE 118 AA; 13292 MW; 7496118E21AD5C41 CRC64;

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alignment_scores:
  Quality: 328.00 Length: 102
  Ratio: 3.859 Gaps: 1
Percent Similarity: 83.333 Percent Identity: 63.725

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alignment_block:

US-09-806-382a-2 x S109_RABIT ..

Align seg 1/1 to: S109_RABIT from: 1 to: 118

```

43 ATGATGACACCTTCCACCAATAGCTGTGAGAGTGGGCGACCCAGAC 92
|||||  |||||||  |||||||  |||||||  |||||||  |||
1 llellelsnlllephenslglnlyserValaIrgvalglYrGaIrgaSpse 17
93 CCGTAACCCAGGGGGAATTCAGAGCTGTGCGAAGATCTGCAAAATT 142
|||||  |||||||  |||||||  |||||||  |||||||  |||
17 lleuSerGlnlysglnlphelysglnleuValaIglInlysglnleuHsaAsp 34
143 TTCTCAAGAGAGGAGATAGAAATGAAAGTCAAGACATCATGAG 192
|||||  |||||||  |||||||  |||||||  |||||||  |||
34 heLeuylsYsglnAlaIrgaSpdluYsaIleAsnArlleMeGln 50
193 GACCTGACACCAATAGCGACAGACAGCTGTGAGAGTTCATCAT 242
|||||  |||||||  |||||||  |||||||  |||||||  |||
51 AspleuAsphrlnsnglnAspYsglnleuSerPhegluIphreValaIl 67
243 GCGTATGCGAGGCTTAACCTGGGCTCCACGAGAGATGACAGAGGT 291
|||||  |||||||  |||||||  |||||||  |||||||  |||
67 eleuMeAlaIrgleuValaIhSaIaSerHsglnlMeHnIlsYsaAsn 84
292 ....GACGAGGGCCCTGGCCACCATAGCCAGGCTCGGGGAGGCG 336
|||||  |||||||  |||||||  |||||||  |||||||  |||
84 laPrHnIsaPhrlnsGlnlyHsSerHsglnYrGlnleuGlyGlySer 100
337 ACCCCC 342
|||
101 G1yPro 102

```

seq_name: SwissProt_40:M126_CHICK

seq_documentation_block:
ID M126_CHICK STANDARD; PRT; 119 AA.

```

AC P28318:
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ProteIn MRP-126.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN SEQUENCE FROM N.A.
RP STRAIN=WHITE LEGHORN; TISSUE=Bone marrow;
RX MEDLINE=92195690; PubMed=1549365;
RA Nakano T., Graf T.;
RT "Identification of genes differentially expressed in two types of
  v-myb-transformed avian myelomonocytic cells.";
RL Oncogene 7:527-534(1992).
CC -! TISSUE SPECIFICITY: EXPRESSED IN V-MYB-TRANSFORMED MYELOMONOCYTIC
  CELLS.
CC -! SIMILARITY: BELONGS TO THE S-100 FAMILY.

```

```

CC -! SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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```

EMBL: X61200; -, NOT_ANNOTATED_CDS.

```

DR HSSP; P04271; 1UW0.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_CABP.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding.
FT CA_BIND 29 42 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 72 83 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
SO SEQUENCE 119 AA; 14065 MW; 2D268DAF6309AD7A CRC64;

```

```

alignment_scores:
  Quality: 216.00 Length: 103
  Ratio: 2.734 Gaps: 2
Percent Similarity: 76.699 Percent Identity: 45.631

```

alignment_block:

US-09-806-382a-2 x M126_CHICK ..

Align seg 1/1 to: M126_CHICK from: 1 to: 119

```

13 ATGTCGAGCTGGAGACCAACATAGACCATATCATCAACACTTCCACCA 62
|||||  |||||||  |||||||  |||||||  |||||||  |||
11 leuSerGlnleuGlnlysaIaIleAspVallelleAspVallelleAsp 27
63 ATACTGTGAAGCTGGGCGACCCAGACACCTTCAACAGGGGGAATCA 112
|||||  |||  |||  |||||||  |||||||  |||
27 nlyrSerArgArgGlnlysaIrgYsaPhrlnleuThrArgYsglnleuL 44
113 AAGAGCTGTGCGAAAGATCTGCAAAATTTTCTCAAGAGAGAAATGAG 162
|||||  |||||||  |||||||  |||||||  |||||||  |||
44 yslleuLeulleGlnlysglnleuAlaAsnlyrleu...LysHsVallys 59
163 AATGAAGAAGTCATAGACACATCATGAGAGACCTGGACCAAAATGAGA 212
|||||  |||||||  |||||||  |||||||  |||||||  |||
60 AsnGlnValSerlleAspGlnllePheLysAspLeuAspAsnlnLysAs 76
213 CAAGACAGCTGAGCTTCGAGAGATTATCATGATGTCGAGCGAGCTAAC 262
|||||  |||||||  |||  |||  |||||||  |||
76 pGlnGlnleuSerPheglYgluValaIleuLeuIlelleArgValaIhry 93
263 GGGCGCTCCACGAGAAAGATGACAGAG...GGTACGAGGGCCCTGGCCAC 309
|||||  |||||||  |||  |||  |||  |||
93 alAlaThrHnIsGlnHsleuHsPheCysGlnAspHnIsGlnGlnHnIs 109
310 CACCATAG 318
|||
110 GlnHsGln 112

```

seq_name: SwissProt_40:S112_PIG

seq_documentation_block:
ID S112_PIG STANDARD; PRT; 91 AA.

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AC P80310:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcgranulin C (CAGC).
OS S100A12.
GN Sus scrofa (Pig).

```


66 yAlaValSerPheGluPheValValLeuValSerArgValLeuLysT 83
 266 CCTCCACGAGAGATGCAGAG 288
 ::::|::| ::|::|::|
 83 hTAlAhTlSleAspIleHisTlys 90

seq_name: SwissProt_40:S112_RABIT

seq_documentation_block:

ID S112_RABIT STANDARD; PRT; 81 AA.
 AC 077791;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calgranulin C (CAGC) (Fragment).
 GN S100A12.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 [1]

SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-Neutrophils;
 RX MEDLINE=96355278; PubMed=8702688;
 RA Yang Z., Deveser M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
 RA Underwood J.R., Robinson H.C.;
 RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
 RL calgranulin C when incubated with inorganic [35S]sulfate."
 CC J. Biol. Chem. 271:19802-19809(1996).
 CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1 SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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 CC -----

DR EMBL: AF091848; AAC61770.1; -.
 DR HSSP: P04631; 1B4C.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001751; S100_Cabp.
 DR Pfam: PF00036; ehand. 1.
 DR Pfam: PF01023; S_100; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 DR KW Calcium-binding.
 FT NON TER 1 1
 FT CA_BIND 8 21 EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY).
 FT CA_BIND 51 62 EF-HAND 2 (HIGH AFFINITY) (BY
 FT SIMILARITY).
 SQ SEQUENCE 81 AA; 9401 MW; 95E67A209180CB66 CRC64;

alignment_scores:

Quality: 181.50 Length: 81
 Ratio: 2.792 Gaps: 1
 Percent Similarity: 80.247 Percent Identity: 41.975

alignment_block:

US-09-806-382a-2 x S112_RABIT ..

Align seg 1/1 to: S112_RABIT from: 1 to: 81

46 ATCAACACCTTCACCACTACTGTGAAGTGGGACACACACACCT 95
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 1 lIleAsnIlePheHisGlnTyrSerValArgThrGlyHisTyrAspThr 17
 96 GAACGAGGGGGAATTCAAAGAGCTGTGGGAAAGATCTGCAAAATTTTTC 145
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 17 uSerLysCysGluLeuLysLysLeuIleThrThrGluLeuValAsnThrI 34

146 TCAAGAAAGAGATATGATAAGTCAATAGACACATCATGAGAGAC 195
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 34 lE...LysAsnThrLysAspGlnAlaThrValAspArgIlePheAsp 49
 196 CTGACACCAAAATGCAGACAGCAGCTGTGAGGAGTTCATCATGCT 245
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 50 LeuAspGluAspGlyAspPheHisGlnValAspPheLysGluPheLeuSerIle 66
 246 GATGCGAGGCTAAGCTGTGGCTCCACGAGAGATGCAGAG 288
 ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 66 uLeuAlaSerValLeuValThrAlaHisGluAsnIleHisTlys 80

seq_name: SwissProt_40:S10B_BOVIN

seq_documentation_block:

ID S10B_BOVIN STANDARD; PRT; 91 AA.
 AC P02638;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE S-100 protein, beta chain.
 GN S100B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OX NCBI_TaxID=9913;
 [1]

SEQUENCE.
 RX MEDLINE=79045265; PubMed=710399;
 RA Isobe T., Okuyama T.;
 RT "The amino-acid sequence of S-100 protein (PAP I-b protein) and its
 RT relation to the calcium-binding proteins."
 RL Eur. J. Biochem. 89:379-388(1978).
 RN [2]
 RP REVISIONS TO 1-4.

RX MEDLINE=81236562; PubMed=7250124;
 RA Isobe T., Okuyama T.;
 RT "The amino-acid sequence of the alpha subunit in bovine brain S-100a
 RT protein."
 RL Eur. J. Biochem. 116:79-86(1981).
 RN [3]
 RP SEQUENCE.

RX MEDLINE=85278169; PubMed=4026304;
 RA Marshak D.R., Umekawa H., Waterson D.M., Hidaka H.;
 RT "Structural characterization of the calcium binding protein s100 from
 RT adipose tissue."
 RL Arch. Biochem. Biophys. 240:777-780(1985).
 RN [4]

RP METAL ION-BINDING PROPERTIES.
 RX MEDLINE=84000339; PubMed=6615778;
 RA Baudier J., Gerard D.;
 RT "Ions binding to S100 proteins: structural changes induced by calcium
 RT and zinc on S100a and S100b proteins."
 RL Biochemistry 22:3360-3369(1983).
 RN [5]

RP CADMIUM-BINDING STUDIES.
 RX MEDLINE=91248136; PubMed=2039467;
 RA Donato H. Jr., Mani R.S., Kay C.M.;
 RT "Spectral studies on the cadmium-ion-binding properties of bovine
 RT brain S-100b protein."
 RL Biochem. J. 276:13-18(1991).
 RN [6]

RP STRUCTURE BY NMR.
 RX MEDLINE=96398693; PubMed=8805590;
 RA Kilby P.M., van Eldik L.J., Roberts G.C.K.;
 RT "The solution structure of the bovine S100b protein dimer in the
 RL calcium-free state."
 CC -1- FUNCTION: WEARILY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY.
 CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
 CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM

Quality: 172.50 Length: 87
Ratio: 2.500 Gaps: 1
Percent Similarity: 79.310 Percent Identity: 39.080

alignment_block:

US-09-806-382A-2 x S10B_HUMAN ..

Align seg 1/1 to: S10B_HUMAN from: 1 to: 91

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16 TCGCAGCTGGAAAGCAGACATAGACACATCATCATCAACCTTCCACCAATA 65
|||||:|||||: : : : : : : : : : : : : : : : : : : : : : : : :
1 SerGluLeuGluLysAlaMetValAlaLeuLeuLeuAspValPheHisGlnTy 17
66 CTCTGTGAAGCTGGGGCACCAGACACCTTGACACGAGGGGAATTCAAG 115
|||||: : : : : : : : : : : : : : : : : : : : : : : : :
17 rSerGlyArgGluGlyAspLysHisLysLeuLysLysSerGluLeuLysG 34
116 ACCTGGTGGCAAAAGATCTGCAAAATTTTCTCAAGAGAGAGATAGAGAT 165
|||||: : : : : : : : : : : : : : : : : : : : : : : : :
34 LuLeuLeuAsnAsnGluLeuSerHisPheLeu..GluGluLeuLysGlu 49

166 GAAAGAGTCATAGAACACATCATGAGAGACCTTGACACCAATGACAGCAA 215
: : : : : : : : : : : : : : : : : : : : : : : : :
50 GlnGluValValAlaAspLysValMetGluThrLeuAspAsnAspGlyAspG 66
216 GCAGCTGAGCTTCGAGAGAGTTTCATGCTGATGCGGAGGCTAACCCTGGG 265
: : : : : : : : : : : : : : : : : : : : : : : : :
66 yGluCysAspPheGlnGluPheMetAlaPheValAlaMetValThrThra 83

266 CCTCCACAGAG 276
|| |||||
83 lacYshHsglu 86

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seq_name: SwissProt_40:S10B_MOUSE

seq_documentation_block:

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ID S10B_MOUSE STANDARD; PRT; 91 AA.
AC P50114;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE S-100 protein, beta chain.
GN S100B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=93388628; PubMed=8376406;
RA Jiang H., Shah S., Hill D.C.;
RT "Organization, sequence, and expression of the murine S100 beta gene.
RT Transcriptional regulation by cell type-specific cis-acting
RT regulatory elements."
RL J. Biol. Chem. 268:20502-20511(1993).
CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-
CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
CC ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
CC ONE ALPHA AND ONE BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL: L22144; AA03075.1; -.
DR HSSP: P04631; 1B4C.
DR MGD: MGI:98217; S100b.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_CABP.
DR Pfam: PF00036; ehand.1.
DR Pfam: PF01023; S_100; 1.
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00303; S100_CABP; 1.
KW Calcium-binding; Zinc; Metal-binding.
FT INIT MET 0 0
FT CA_BIND 18 31 BY SIMILARITY.
FT CA_BIND 61 72 EF-HAND 1 (LOW AFFINITY).
FT CA_BIND 91 105 EF-HAND 2 (HIGH AFFINITY).
SQ SEQUENCE 91 AA; 10597 MW; 2378A8B8F81C94D CRC64;

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alignment_scores:

Quality: 171.50 Length: 87
Ratio: 2.522 Gaps: 1
Percent Similarity: 78.161 Percent Identity: 39.080

alignment_block:

US-09-806-382A-2 x S10B_MOUSE ..

Align seg 1/1 to: S10B_MOUSE from: 1 to: 91

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16 TCGCAGCTGGAAAGCAGACATAGAGACCATCATCAACCTTCCACCAATA 65
|||||:|||||: : : : : : : : : : : : : : : : : : : : : : : : :
1 SerGluLeuGluLysAlaMetValAlaLeuLeuLeuAspValPheHisGlnTy 17
66 CTCTGTGAAGCTGGGGCACCAGACACCTTGAAACGAGGGGAATTCAAG 115
|||||: : : : : : : : : : : : : : : : : : : : : : : : :
17 rSerGlyArgGluGlyAspLysHisLysLeuLysLysSerGluLeuLysG 34
116 AGCTGGTGGCAAAAGATCTGCAAAATTTTCTCAAGAGAGAGATAGAGAT 165
|||||: : : : : : : : : : : : : : : : : : : : : : : : :
34 LuLeuLeuAsnAsnGluLeuSerHisPheLeu..GluGluLeuLysGlu 49

166 GAAAGAGTCATAGAACACATCATGAGAGACCTTGACACCAATGACAGCAA 215
: : : : : : : : : : : : : : : : : : : : : : : : :
50 GlnGluValValAlaAspLysValMetGluThrLeuAspGluLysGlyAspG 66
216 GCAGCTGAGCTTCGAGAGAGTTTCATGCTGATGCGGAGGCTAACCCTGGG 265
: : : : : : : : : : : : : : : : : : : : : : : : :
66 yGluCysAspPheGlnGluPheMetAlaPheValAlaMetValThrThra 83

266 CCTCCACAGAG 276
|| |||||
83 lacYshHsglu 86

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seq_name: SwissProt_40:S10B_RAT

seq_documentation_block:

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ID S10B_RAT STANDARD; PRT; 91 AA.
AC P04631;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE S-100 protein, beta chain.
GN S100B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85037924; PubMed=6093041;
RA Kuwano R., Usui H., Maeda T., Fukui T., Yamanari N., Ohtsuka E.,

```

RA Ikehara, Takahashi Y.;
RT "Molecular cloning and the complete nucleotide sequence of cDNA to
RT mRNA for S-100 protein of rat brain."
RL Nucleic Acids Res. 12:7455-7465(1984).
RN [2]
RP SEQUENCE FROM N.A.
RA Kuwano R., Usui H., Maeda T., Araki K., Kurihara T., Yamakuni T.,
RA Ohtsuka E., Ikehara M., Takahashi Y.;
RT "Molecular cloning and nucleotide sequences of cDNA and genomic DNA
RT for alpha and beta subunits of S100 protein."
RL Taniguchi Symp. Brain Sci. 19:243-255(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-91359841; Pubmed-1653388;
RA Maeda T., Usui H., Araki K., Kuwano R., Takahashi Y., Suzuki Y.;
RT "Structure and expression of rat S-100 beta subunit gene."
RL Brain Res. Mol. Brain Res. 10:193-202(1991).
RN [4]
RP SEQUENCE OF 5-91 FROM N.A.
RX MEDLINE-87137648; Pubmed-3818655;
RA Dunn R., Landry C., O'Hanlon D., Dunn J., Alliore R., Brown I.,
RA Marks A.;
RT "Reduction in S100 protein beta subunit mRNA in C6 rat glioma cells
RT following treatment with anti-microtubular drugs."
RL J. Biol. Chem. 262:3562-3566(1987).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE-96387197; Pubmed-8794737;
RA Drohat A.C., Amburgey J.C., Abildgaard F., Starich M.R.,
RA Baldissari D.M., Weber D.J.;
RT "Solution structure of rat apo-S100(beta beta) as determined by NMR
RT spectroscopy."
RL Biochemistry 35:11577-11588(1996).
RN [6]
RP STRUCTURE BY NMR.
RX MEDLINE-98153156; Pubmed-9485423;
RA Drohat A.C., Baldissari D.M., Rustandi R.R., Weber D.J.;
RT "Solution structure of calcium-bound rat S100(beta beta) as
RL determined by nuclear magnetic resonance spectroscopy."
RN Biochemistry 37:2729-2740(1998).
RN [7]
RP STRUCTURE BY NMR.
RX MEDLINE-99226808; Pubmed-10211826;
RA Drohat A.C., Tiandra N., Baldissari D.M., Weber D.J.;
RT "The use of dipolar couplings for determining the solution structure
RT of rat apo-S100b."
RL Protein Sci. 8:800-809(1999).
CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-
CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
CC ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
CC ONE ALPHA AND ONE BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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CC -----
DR EMBL; X01090; CAA25567.1; -;
DR EMBL; M54919; AAA42096.1; -;
DR EMBL; S53527; -; NOT_ANNOTATED_CDS;
DR EMBL; G53522; -; NOT_ANNOTATED_CDS;
DR EMBL; M15705; -; NOT_ANNOTATED_CDS;

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DR   PIR; S07357; S07357.
DR   PIR; A26557; A26557.
DR   PDB; 1SYW; 07-DEC-96.
DR   PDB; 1OLK; 11-NOV-98.
DR   PDB; 1B4C; 30-DEC-98.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001751; S100_CaBP.
DR   Pfam; PF00036; ehand; 1.
DR   Pfam; PF01023; S_100; 1.
DR   PROSITE; PS00018; EF_HAND; 1.
DR   PROSITE; PS00303; S100_CaBP; 1.
DR   Calcium-binding; Zinc; Metal-binding; 3D-structure.
KW   Calcium-binding; Zinc; Metal-binding; 3D-structure.
FT   CAT.BIND    0
FT   INT.MET     0
FT   CA.BIND     18   31
FT   CA.BIND     61   72
FT   SEQUENCE    91 AA; 10613 MW; 2378AAB8BF7134D CRC64;
SO

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alignment_scores:

Quality:	168.50	Length:	87
Ratio:	2.478	Gaps:	1
Percent Similarity:	78.161	Percent Identity:	37.931

alignment_block:

US-09-806-382A-2 x S10B-RAT ..

Align seg 1/1 to: S10B-RAT from: 1 to: 91

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16  TCGCAGCTGTGAACCAACATATGAGACCATCATCACACCTTCACCAATA 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1  SerGluLeuGluLysAlaMetValAlaLeuIleAspValPheHisGluTyr 17
66  CTCGTGTGAAGCTGGGGCACCACCACACCCCTTGAAACCAAGGGGAATTCAA 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  TserIlyArgGluGluLysPheLysLeuLysLysSerGluLeuLysG 34
116 ACCTGTGTCGAAAGATCTGCAAAATTTTCTCAAGAGAGAGAAATGAAGAT 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  IuLeuIleAsnHisGluLeuSerHisPheLeu...GluGluIleLysGlu 49
166 GAAAGTGTATAGAACATCATGTGAGAGACCTTGACACAAATGACAGACAA 215
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
50  GlnGluValValAspLysValMetGluThrLeuAspGluAspGluYAsp 66
216 GCAGGTGAGCTTGAGAGGTTGATCATGCTGATGAGGGGAGGCTAACCTGG 265
+:::++:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
66  yLudysAspPheGlnGluPheMetAlaPheValSerMetValThrTrpA 83
266 CCTCCACAGAG 276
|| |||||
83  LacYSHISGlu 86

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seq_name: SwissProt_40:S10E_HUMAN

seq_documentation_block:

ID	S10E_HUMAN	STANDARD;	PRT;	95 AA.
AC	P25815;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	S-100P protein.			
GN	S100P OR S100E.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=92339442; PubMed=1633809;			
RA	Becker T., Geike V., Kube E., Weber K.;			
RT	"S100P, a novel Ca(2+)-binding protein from human placenta. cDNA cloning, recombinant protein expression and Ca2+ binding			

OM of: US-09-806-382a-2 to: SPTREMBL_19:* out-format : pfs

Date: Sep 9, 2002 3:24 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=firmat_n2p.model -DEV=xlp
-O=/cgr2_1/USPRO_pool/US09806382/runtal_09092002.143849_15535/app-query.fasta_1.752
-DB=SPTREMBL_19 -OFMT=fastan -SUFFIX=rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPT=0.000 -LOOPTXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=bloms62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NOM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09806382.eccml_1_279 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-806-382a-2
Query length: 345
Database: SPTREMBL_19:*
Database sequences: 362222
Database length: 172994929
Search time (sec): 104.890000

Score list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SP-rodent:Q90VR5	+	256.50	479.27	2.9e-18	83 Q90VR5 rattus sp. calprotectin
SP-vertebrate:Q93395	+	179.50	2.9e-10	101 Q93395 salvelinus fontinalis (b	
SP-rodent:Q92573	+	172.50	3.21.70	1.6e-09	92 Q92573 cricetus griseus (ch
SP-rodent:Q91V77	+	156.50	291.67	7.1e-08	94 Q91V77 m. 11 days embryo cda
SP-human:Q9NR83	+	155.50	289.45	9.1e-08	98 Q9NR83 homo sapiens (human). s
SP-mammal:Q9TR16	+	154.50	290.50	1.1e-07	70 Q9TR16 bos taurus (bovine). cor
SP-human:Q94U01	+	154.50	280.86	1.3e-07	213 Q94U01 homo sapiens (human). d
SP-human:Q01J20	+	154.00	271.08	1.6e-07	591 Q01J20 homo sapiens (human). f
SP-human:Q94U02	+	154.00	269.78	1.6e-07	687 Q94U02 homo sapiens (human). d
SP-rodent:Q9D3M4	+	152.50	284.21	1.9e-07	94 Q9D3M4 mus musculus (mouse). s
SP-mammal:Q9TV56	+	148.00	275.20	5.5e-07	101 Q9TV56 canis familiaris (dog).
SP-rodent:Q9U108	+	142.50	267.07	2.0e-06	79 Q9U108 mus musculus (mouse). s
SP-human:Q03331	+	141.00	240.57	3.9e-06	1218 Q03331 homo sapiens (human). f
SP-vertebrate:Q9PSF6	+	140.50	262.02	3.3e-06	92 Q9PSF6 ictalurus punctatus (cha
SP-rodent:Q9R2B7	+	135.00	252.05	1.2e-05	89 Q9R2B7 rattus norvegicus (rat).
SP-vertebrate:Q9YH57	+	135.00	244.32	1.3e-05	217 Q9YH57 rana catesbeiana (bull f
SP-human:Q9ICJ1	+	133.00	257.74	1.7e-05	30 Q9ICJ1 homo sapiens (human). cal
SP-human:Q9NBG3	+	118.00	203.47	0.0009	495 Q9NBG3 homo sapiens (human). t
SP-rodent:Q96FQ6	+	117.00	217.21	0.0009	103 Q96FQ6 mus musculus (mouse). s
SP-rodent:Q91X65	+	111.50	209.14	0.0033	80 Q91X65 mus musculus (mouse). s
SP-human:Q941E2	+	106.00	197.96	0.0125	89 Q941E2 homo sapiens (human). psc
SP-human:Q9HCY8	+	103.50	191.94	0.0232	104 Q9HCY8 homo sapiens (human). s
SP-vertebrate:Q9ST59	+	100.50	170.44	0.0582	652 Q9ST59 drosophila melanogaste
SP-vertebrate:Q9VSH4	+	100.50	169.80	0.0587	702 Q9VSH4 drosophila melanogaste
SP-rodent:Q9D208	+	95.50	177.02	0.1570	104 Q9D208 mus musculus (mouse). 11
SP-rodent:Q9D1D8	+	95.50	174.57	0.1570	104 Q9D1D8 mus musculus (mouse). 11
SP-rodent:Q9D708	+	95.00	157.02	0.2261	940 Q9D708 mus musculus (mouse). 23
SP-human:Q00405	+	92.00	156.30	0.4352	535 Q00405 homo sapiens (human). f
SP-plant:Q38873	+	92.00	151.42	0.4634	940 Q38873 arabidopsis thaliana (m
SP-human:Q96QC0	+	91.50	151.85	0.5003	638 Q96QC0 homo sapiens (human). f
SP-rodent:Q87314	+	91.00	171.70	0.4430	73 Q87314 oryctolagus cuniculus (r
SP-invertebrate:Q18887	+	89.50	156.09	0.7475	320 Q18887 caenorhabditis elegans
SP-virus:Q9PWX1	+	89.00	147.68	0.9275	759 Q9PWX1 human herpesvirus 6p. d
SP-organelle:Q21351	+	88.50	154.53	0.9459	309 Q21351 ethadra herklotzi. nadh
SP-plant:Q93759	+	88.50	149.86	1.00	530 Q93759 arabidopsis thaliana (m
SP-plant:Q42438	+	88.50	149.81	1.01	533 Q42438 arabidopsis thaliana (m
SP-virus:Q9W9G4	+	88.00	147.20	1.16	647 Q9W9G4 human herpesvirus 6. d
SP-bacteria:Q9REK6	+	87.50	158.81	1.11	152 Q9REK6 micrococcus luteus (micr
SP-mammal:Q9T5B1	+	87.00	166.69	1.12	55 Q9T5B1 bos taurus (bovine). cal

SP-rodent:Q91WZ7 + 84.50 149.74 2.38 227 | Q91WZ7 rattus norvegicus (ra
SP-plant:Q23184 + 83.50 150.54 2.92 167 | Q23184 arabidopsis thaliana
SP-human:Q96BA4 + 83.00 149.15 3.31 176 | Q96BA4 homo sapiens (human).
SP-human:Q95616 + 83.00 145.51 3.47 268 | Q95616 homo sapiens (human).

seq_name: SP-rodent:Q90VR5

seq_documentation_block:
ID Q90VR5 PRELIMINARY; PRT; 83 AA.
AC Q90VR5;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE CALPROTECTIN LARGER COMPONENT MRP-14 (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9539365; PubMed=7665986;
RA Yui S., Mikami M., Yamazaki M.;
RT "Purification and characterization of the cytotoxic factor in rat
RT peritoneal exudate cells: its identification as the calcium binding
RT protein complex, calprotectin."
RL J. Leukoc. Biol. 58:307-316(1995).
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR HSSP: P02638; IMHO.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_CABP.
DR Pfam: PF00036; efhand; 1.
DR PROSITE: PS00303; S100_CABP; 1.
KW Calcium-binding.
SQ SEQUENCE 83 AA; 9811 MW; 2E1204E5DD72CA18 CRC64;

alignment_scores:
Quality: 256.50 Length: 83
Ratio: 3.664 Gaps: 1
Percent Similarity: 84.337 Percent Identity: 60.241

alignment_block:
US-09-806-382a-2 x Q90VR5 ..

Align seg 1/1 to: Q90VR5 from: 1 to: 83

88 GACACCCGACGAGGAGGATTCAGAGAGCTGGGCAAGATTCGA 137
|||||
1 ASPRTLEASNLVSALAGLURHELYSGILMEYVALSNLSARLYR 17
138 AATTTTCTCAAGAGAGAGATTAAGATGAAGATGATGACATCA 187
|||||
17 CASHPELEULSARGLULSARGNSGLNLSLLEULALRGSLLEM 34
188 TGAGAGACCTGACACAAATGACACAAAGACGCTGAGAGACTTC 237
|||||
34 ETGLASPLLEASLPRTHASNGINLSRPSNGINLSERPHESGLNLS 50
228 ATCATGCGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 287
|||||
51 MEKTEGASMEGLYLSLLEPHELEHLEACYSNLSLULSGLNLSGL 67
288 GGGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 336
|||||
67 WASHASPRG...ARGGLNLSARHNSLARGNLSGLLYLGLYUGSLY 82
seq_name: SP-vertebrate:Q93395
seq_documentation_block:
ID Q93395 PRELIMINARY; PRT; 101 AA.
AC Q93395;
DT 01-NOV-1998 (TREMREL. 08, Created)

```
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE S100-LIKE CALCIUM BINDING PROTEIN.
GN S100.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Procranchiopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVULATORY OVARY;
RX MEDLINE=20534789; PUBMED=11080585;
RA Bohe J., Goetz F.W.;
RT "A S100 homologue mRNA isolated by differential display PCR is down-
RT regulated in the brook trout (Salvelinus fontinalis) post-ovulatory
RT ovary."
RL Gene 257:187-194(2000).
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL: AF077613; AAC28367.1; -.
DR HSP; P02633; 41CB.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_CaBP.
DR Pfam: PF00036; efhand.1.
DR Pfam: PF01023; S_100; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE: PS00303; S100_CaBP.1.
KW Calcium binding.
SQ SEQUENCE 101 AA; 11285 MW; BF45582FF9279D0A CRC64;
```

```
alignment_scores:
  Quality: 179.50      Length: 87
  Ratio: 2.601        Gaps: 1
  Percent Similarity: 79.310      Percent Identity: 43.678
```

```
alignment_block:
US-09-806-382A-2 x 093395 ..
```

```
Align seg 1/1 to: 093395 from: 1 to: 101
```

```
16 TCGCAGCTGGAACGACATAGAGACCATCATCAACACTTCCACCAATA 65
|||||
3 SerGlnLeuGlnSerMetGlnSerLeuIleThrValPheHisArgTyr 19
|||||
66 CTCTGTGAAGCTGGGGCCACCCAGACCCCTGACACGAGGGGAATTCAAG 115
|||||
19 rAlaAspLysAspGlyAspCysAsnThrLeuSerLysLysGlnLeuLysG 36
|||||
116 AGCTGGTGCAGAAAGATCTGCAAAATTTCTCAAGAAGAGAAATTAAGAT 165
|||||
36 IuLeuMetGlnThrGlnLeuAlaSerPheLeuLysSerGln...LysAsp 51
|||||
166 GAAAGGTCATAGAACATCATGAGAGACCTGAGACACAATGCGAGACAA 215
|||||
52 ProAlaIleAlaLeuSerThrIleMetLysAspLeuAspGlnsnGlyAspG 68
|||||
216 GCAGCTGAGCTTGGAGAGTTTCATCATGCTGATGCGAGGAGCTAACCTGGG 265
|||||
68 yLysValSerPheGlnIuPheValSerLeuValIaGlyLeuSerIleA 85
|||||
266 CCTGCCCGCAGAG 276
||
85 IaCysGlnGln 88
```

```
seq_name: sp_rodent:Q925T3
```

```
seq_documentation_block:
```

```
ID 0925T3 PRELIMINARY; PRT; 92 AA.
AC 0925T3.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
```

```
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE S100B.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuge O., Yamakawa Y., Nishijima M.;
RT "Enhancement of transport-dependent decarboxylation of
RT phosphatidylserine by S100B protein in permeabilized Chinese hamster
RT ovary cells."
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL: AB056121; BAB43945.1; -.
SQ SEQUENCE 92 AA; 10749 MW; AF50107EC2BEDF6B CRC64;
```

```
alignment_scores:
  Quality: 172.50      Length: 88
  Ratio: 2.537        Gaps: 1
  Percent Similarity: 77.273      Percent Identity: 38.636
```

```
alignment_block:
US-09-806-382A-2 x Q925T3 ..
```

```
Align seg 1/1 to: Q925T3 from: 1 to: 92
```

```
13 ATGTGCGAGCTGGAACGACATAGAGACCATCATCAACACTTCCACCA 62
|||||
1 MetSerGlnLeuGlnLysAlaMetValAlaLeuIleAspIlePheHisG 17
|||||
63 ATACTGTGAAGCTGGGGCCACCCAGACCCCTGACACGAGGGGAATTCA 112
|||||
17 nTyrSerGlyArgGlnGlyAspLysHisLysLeuLysLysSerGlnLeu 34
|||||
113 AAGAGCTGTCGCAAAAGATCTGCAAAATTTCTCAAGAAGAGAAATTAAG 162
|||||
34 yGlnIleIleAsnAsnGlnLeuSerHisPheLeu...GlnGlnIleLys 49
|||||
163 AATGAAAGTCTATGAAACATCATGAGAGACCTGAGACACAATGCGAGA 212
|||||
50 GlnGlnIleValValAlaAspLysValMetGlnThrLeuAspGlnAspG 66
|||||
213 CAAGCACTGAGCTTGGAGAGTTTCATCATGCTGATGCGAGGAGCTAAC 262
|||||
66 pGlyGlnLysAspPheGlnIuPheMetAlaPheValSerMetValThr 83
|||||
263 GGGCCTCCACGAG 276
||
83 hAlaCysHisGln 87
```

```
seq_name: sp_rodent:Q91V77
```

```
seq_documentation_block:
```

```
ID 091V77 PRELIMINARY; PRT; 94 AA.
AC 091V77.
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE 11 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:270008BD09, FULL INSERT SEQUENCE (S100 CALCIUM BINDING PROTEIN
DE A1) (ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610031F03, FULL INSERT SEQUENCE).
GN S100A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
```

RA Atakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagata T., Hara A., Hayatsu N., Hirakuni K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shingaura A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Morimatsu M., Hayashizaki Y.,
RL submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [12]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [13]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [14]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [15]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishise T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [16]
RN
RP SEQUENCE FROM N.A.
RC STRAUSBERG R.;
RL submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [17]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Du X.-J., Cole T.J., Tennis N., Gao X.-M., Kontgen F., Kemp B.E.,
RA Heierhorst J.;
RT "Impaired cardiac contractility without cardiomyopathy in S100A1-
RT deficient mice.";
RL submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK012578; BAR28330.1; -;
DR EMBL: BC005550; AAH05590.1; -;
DR EMBL: AF368423; AAL14436.1; -;
DR EMBL: AK002721; BAR22308.1; -;
SQ SEQUENCE 94 AA: 10505 MW; 708E817BBF36ED15 CRC64;

alignment_scores:	Quality: 156.50	Length: 84
	Ratio: 2.484	Gaps: 1
Percent Similarity:	75.000	Percent Identity: 38.095

US-09-806-382A-2 x Q91V77 ..
Align seg 1/1 to: Q91V77 from: 1 to: 94

[illegible]

seq_name: sp_human:Q9BU83

```

seq_documentation_block:
ID 09B083      PRELIMINARY;      PRT;      98 AA.
AC 09B083;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE S100 CALCIUM-BINDING PROTEIN A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY, ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (FEH-2001) to the EMBL/Genbank/DBJ databases.
CC 1-1 SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; BC002829; AA002829.1; -.
DR HSSP; P30801; IA03.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_Cabp.
DR Pfam; PF01023; S.100; 1.
DR SMART; SM00054; EFP; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN.1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 98 AA; 1117 MW; 56D09548450142A9 CRC64;

```

alignment_scores:		
Quality:	155.50	Length: 87
Ratio:	2.356	Gaps: 2
Percent Similarity:	75.862	Percent Identity: 36.7823

```
alignment_block:
```

Align seg 1/1 to: Q9BU83 from: 1 to: 98

```

1  ATGACCTTGCAAAATGTGCGACGCTGGAAACGCACATATAGACACATCATCA  50
    ||| ||| ||||| |||||:: :: :::::
1  MetMetcs.....SerSerLeuGluGlnAlaLeuAlaValLeuValTh  15
51  CACCTTCACCAACAATACTCTGTGGAAGCTGAGGGACCCACCGACACCTGTGACC  100

```

```

15 rThPheN1s1yStySerCysGlnGluAspLysPheLysLeuSerL 32
101 AGGGGGAATTCAGAGAGCTGGTGGAGAAAGATCTGCAAAATTTTCTCAAG 150
32 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
32 ysgLysMetLysGluLeuLeuHisLysGluLeuProSerPheVal... 47
151 AAGGAGATATAGAGATGAAAGTCAATAGACATCATCATGAGAGAGCTGGG 200
48 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
48 GylGluValAspGlnGluGlyLeuLysLysLeuMetCylSerLeuAs 64
201 CACAAATGACAGACAGAGCTGAGCTTCGAGGATTCATCATGCTGATGG 250
64 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 pGluAspSerAspGlnGlnValAspPheGlnGluTyrAlaValPheLeuA 81
251 CGAGGCTAAC 261
81 :|||||
81 lateuilethr 84
seq_name: sp_mammal:Q9TR16

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```

seq_documentation_block:
ID Q9TR16 PRELIMINARY; PRT; 70 AA.
AC Q9TR16:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CORNEA-ASSOCIATED ANTIGEN, CO-AG-CALGRANULIN C HOMOLOG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE=96181454; PubMed=8603881;
RA Liu S.H.; Gottsch J.D.;
RT "Amino acid sequence of an immunogenic corneal stromal protein.";
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR HSSP; P02638; IMHO.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_Cabp.
DR Pfam; PF01023; S_100; 1..
SQ SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;

```

```

alignment_scores:
Quality: 154.50 Length: 68
Ratio: 2.809 Gaps: 2
Percent Similarity: 80.882 Percent Identity: 48.529

```

alignment_block:

US-09-806-382A-2 x Q9TR16 ..

Align seg 1/1 to: Q9TR16 from: 1 to: 70

```

16 TGGCAGCTGGAAAGCAACATAGACATCATCAACCTTCACCAATA 65
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ThrLysLeuGluAspHisLeuGluLysLeuLeuHisLeuHisGlnTyr 17
66 CTCTGTGAAGCTGGGGCAGACCCGACAGCCCTGAGGAGGGGAATTCAAG 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 rSerValAlaGlyHisPheAspThrLeuAsnLysArgGluLeuLysG 34
116 AGCTGTGCGAAAGATCTGCAAAATTTTCTCAAGAGAGAGAAATAGAT 165
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 lntleuilethrLysGluLeuProLysThrLeu...GlnAsnThrLysasp 49
166 GAAAGGCTATGAGACATCATGAGAGAGCTGGACACAAATTCAGAGACA 215
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
50 GlnProThrLysAspLysLysPheGlnAspLeuAsp.....AlaAspLys 64

```

216 GCAG 219
:|||||
64 slys 65

seq_name: sp_human:Q9H4U1

```

seq_documentation_block:
ID Q9H4U1 PRELIMINARY; PRT; 213 AA.
AC Q9H4U1:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DJ14N1.2 (NOVEL S-100/TCABP TYPE CALCIUM BINDING DOMAIN PROTEIN,
DE SIMILAR TO TRICHOHYALIN) (FRAGMENT).
GN DJ14N1.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; AL356504; CAC13173.1; -.
DR HSSP; P02638; 1CFP.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_Cabp.
DR Pfam; PF01023; S_100; 1.
DR SMART; SM00054; EFh; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON TER 213
SQ SEQUENCE 213 AA; 24340 MW; B8C6E0810098E7D2 CRC64;

```

```

alignment_scores:
Quality: 154.50 Length: 114
Ratio: 2.033 Gaps: 3
Percent Similarity: 66.667 Percent Identity: 32.456

```

alignment_block:

US-09-806-382A-2 x Q9H4U1 ..

Align seg 1/1 to: Q9H4U1 from: 1 to: 213

```

13 ATGTGCGAGCTGGAAGCAACATAGACATCATCAACCTTCACCA 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetThrAspLeuLeuArgSerValAlaThrValIleAspAlaPheTyrLys 17
63 ATACTGTGTAAGCTGGGGCAGACCCGACAGCCCTGAGACAGGAGGAATCA 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 sTyrThrLysGlnAspLysGlyLysGlyThrLeuSerLysGlyGluLeu 34
113 AAGAGCTGGTGGAAAGATCTGCAAAATTTTCTCAAGAGAGAGATAG 162
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 ysgLysLeuLeuGluLysGluLeuHisPheValIleLysAsnProAsp... 49
163 AATGAAAGGTCATAGAACATCATGAGAGCTGAGAGCAACAAATGACAG 212
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
50 AspProAspThrValAspValIleMetHisMetLeuAspArgAspHisAs 66
213 CAAGCAGCTAGCTTCGAGAGATTCATCATGCTGATGGCAGGAGTAACCT 262
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 pArgArgLeuAspPheThrGluPheLeuLeuMetIlePheLysLeuThrM 83
263 GG.....GCTCCACGAG 276
83 eAlaCysAsnLysValLeuSerLysGluTyrCysLysAlaSerGlySer 99
277 AAGATGACGAGGAGGTGACGAGGCGCTGGCCACACCATTAAG 318
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
100 LysLysHisArg.....ArgGlyHisArgHisGln 109

```



```
alignment_scores:
    Quality: 152.50      Length: 84
    Ratio: 2.421         Gaps: 1
Percent Similarity: 75.000 Percent Identity: 36.905
```

Ratio:	2.056	Gaps:	33.3333
Percent Similarity:	75.000	Percent Identity:	33.3333

alignment_block:

US-09-806-382A-2 x Q05331 ..

Align seg 1/1 to: Q05331 from: 1 to: 1218

```

13 ATGTGACAGCTGGAGACGACATAGACCATCATCAGACCTTCACCA 62
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 MetSerThrIleuLeuValPheIlePheAlaIleIleAsnIleuPheAsnG1 17
63 ATACTGTGAAGCTGGGGACCCACACCCCGAAGGAGGGAATTC 112
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
17 uTySerLysLysAspLysAsnThrAspThrLeuSerLysGluLeuL 34
113 AAGAGCTGTGCGAAAAGATCTGCAAAATTTCTCAAGAAGAGAAATAG 162
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
34 ysgIuLeuLeuGluLysGluPheArgGlnIleuLysAsnProasp... 49
163 AATGAAAAGTCTATAGACACATCATGAGAGCTTGACACAAATGCAGA 212
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
50 AspProAspMetValAspValPheMetAspHisIleuAspHisAs 66
213 CAAGCAGCTGAGCTTGAGAGATTCATCATGCGATGCGAGGCTTAACCT 262
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 nysLysIleAspPheThrGluPheLeuLeuMetValPheLysLeuAlaG 83
263 GGGCCTCCACGAGAGATGCAC...GAGGCTGACGAGGCGCCCTGACAC 309
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
83 InAlaTyrrTyrgIuSerThrArgLysGluAsnLeuProIleSerGlyHis 99
310 CACCATAG 318
|||||
100 LysHisArg 102

```

seq_name: sp_vertibrate:Q9PSF6

seq_documentation_block:

```

ID Q9PSF6 PRELIMINARY; PRT; 92 AA.
AC Q9PSF6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ICHTHALCIN.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
OC Siluriformes; Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-9437615; PubMed-8090068;
RA Bettini E., Porta A.R., Dahmen N., Wang H., Margolis F.L.;
RT "Expressed sequence tags (EST) identify genes preferentially expressed
RT in catfish chemosensory tissues."
RL Brain Res. Mol. Brain Res. 23:285-291(1994).
CC -1 SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR HSSP; P30801; 1A03.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_Cabp.
DR Pfam; PF000036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding.
SQ SEQUENCE 92 AA; 10022 MW; E04875D0C9921C50 CRC64;

```

alignment_scores:

Quality: 140.50 Length: 90
Ratio: 2.129 Gaps: 1
Percent Similarity: 73.333 Percent Identity: 33.333

alignment_block:

US-09-806-382A-2 x Q9PSF6 ..

Align seg 1/1 to: Q9PSF6 from: 1 to: 92

```

13 ATGTGACAGCTGGAGACGACATAGACCATCATCAGACCTTCACCA 62
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 MetSerAspLeuGluLysGluMetAlaLeuLeuIleSerThrPheHisLys 17
63 ATACTGTGAAGCTGGGGACCCACACCCCGAAGGAGGGAATTC 112
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
17 sTySerIylGluGluLysAspLysCysThrIleThrLysGluLeuL 34
113 AAGAGCTGTGCGAAAAGATCTGCAAAATTTCTCAAGAAGAGAAATAG 162
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
34 yAspLeuLeuThrLysGluLeuGluLysAlaPhe...GlyAsnCysSer 49
163 AATGAAAAGTCTATAGACACATCATGAGAGCTTGACACAAATGCAGA 212
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
50 AspGlnAlaThrIleAspLysIlePheLysAspLeuAspThrAsnAlaAs 66
213 CAAGCAGCTGAGCTTGAGAGATTCATCATGCGATGCGAGGCTTAACCT 262
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 pGlyValValAspPheGluGluTyrrAlaThrMetValAlaCysThrThrm 83
263 GGGCCTCCACGAGAGATG 282
|||||
83 eTleuCysAsnLysSerLeu 89

```

seq_name: sp_rudent:Q9R2B7

seq_documentation_block:

```

ID Q9R2B7 PRELIMINARY; PRT; 89 AA.
AC Q9R2B7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCYCLIN (CALCIUM BINDING PROTEIN).
GN CACY OR S100A6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WISTAR;
RA Konrad L., Gabius H.J., Aumüller G.;
RT "Sequence and expression study of calycclin in the rat testis."
RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-WISTAR;
RA Ito M., Kizawa K.;
RT "Expression of S100 genes in hair follicle epithelium."
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; AJ132717; CAB42002.1; -.
DR EMBL; AF140232; AAK28306.1; -.
DR HSSP; P30801; 1A03.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_Cabp.
DR Pfam; PF000036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Cyclin.
SQ SEQUENCE 89 AA; 10035 MW; 2AA1A4163D57DC87 CRC64;

```

alignment_scores:

Quality: 135.00 Length: 94
Ratio: 2.213 Gaps: 2
Percent Similarity: 64.894 Percent Identity: 31.915

100

```
1 LysGluAsnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAATATGCAGACAAGACAGCTGAGCTTCGAGAGATTATCATGTCGATGG 250
17 pThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetA 34
251 CGAGGCTTAACCTGGGCTCCACGAGAGATGCACGAGGGTGACGAGGCG 300
34 laArgLeuThrTrpAlaSerHisGluLysMetHisGluGlyAspGluGly 50
301 CCTGGCCACACCATATAGCCAGGCTCGGGGAGGCGACCCCG 342
|||||
51 ProGlyHisHisHisLysProGlyLeuGlyGluGlyThrPro 64
seq_name: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:ABB25051
seq_documentation_block:
ID ABB25051 standard; Protein: 64 AA.
AC ABB25051;
XX
XX 23-JAN-2002 (first entry)
DT
XX
DE Protein #7050 encoded by probe for measuring heart cell gene expression.
XX
XX Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
XX Homo sapiens.
OS
XX
XX WO200157274-A2.
PN
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00666.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488899/53.
DR
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
XX Claim 15; SEQ ID No 26821; 530pp; English.
PS
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease.
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIDO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 64 AA:
64
alignment_scores:
6
4
```

```
Quality: 351.00 Length: 64
Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-806-382A-2 x ABB25051 ..
Align seg 1/1 to: ABB25051 from: 1 to: 64
151 AAGAGATTAAGATGAAAAGTTCATAGACACATATATGAGAGCTGGA 200
|||||
1 LysGluAsnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAATATGCAGACAAGACAGCTGAGCTTCGAGAGATTATCATGTCGATGG 250
17 pThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetA 34
251 CGAGGCTTAACCTGGGCTCCACGAGAGATGCACGAGGGTGACGAGGCG 300
34 laArgLeuThrTrpAlaSerHisGluLysMetHisGluGlyAspGluGly 50
301 CCTGGCCACACCATATAGCCAGGCTCGGGGAGGCGACCCCG 342
|||||
51 ProGlyHisHisHisLysProGlyLeuGlyGluGlyThrPro 64
seq_name: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:AAM61792
seq_documentation_block:
ID AAM61792 standard; Protein: 64 AA.
XX
XX AAM61792;
AC
XX
XX 05-NOV-2001 (first entry)
DT
XX
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 33897.
DE
XX
XX Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
XX Homo sapiens.
OS
XX
XX WO200157275-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00667.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483446/52.
DR
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
XX Example 4; SEQ ID NO: 33897; 650pp + Sequence Listing; English.
PS
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
```

CC the probes of the invention.

XX Sequence 64 AA;

alignment_scores:

Quality:	351.00	Length:	64
Ratio:	5.484	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-806-382A-2 x AAM61792 ..

Align seg 1/1 to: AAM61792 from: 1 to: 64

```
151 AAGGAGATAGAAATGAAGAAGTCATAGAACATCATGAGAGACCTGGA 200
|||||
1  LysGluAsnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAAATGCAGACAGCAGCTGAGCTTCGAGAGATTCAATCATGCTGATGG 250
|||||
17 pThrAsnAlaAspLysGlnLeuSerPheGluGlnPheIleMetLeuMetA 34
251 CGAGGCTTAACCTGGGCTCCACGAGAGATGCACGAGGGTGACGAGGGC 300
|||||
34 IaArgLeuThrTyrPalaSerHisGluLysMetHisGluGlnLysAspGluGly 50
301 CCGGGCCACACCATTAAGCAGGCTCGGGGAGGAGGACCCCC 342
|||||
51 ProGluHisHisHisLysProGlyLeuGlyGluGlyThrPro 64
```

seq_name: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT: AAM74591

seq_documentation_block:

ID AAM74591 standard; Protein; 64 AA.

AC AAM74591;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34897.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

XX 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US00668.

PF 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 34897; 658bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

XX Sequence 64 AA;

alignment_scores:

Quality:	351.00	Length:	64
Ratio:	5.484	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-806-382A-2 x AAM74591 ..

Align seg 1/1 to: AAM74591 from: 1 to: 64

```
151 AAGGAGATAGAAATGAAGAAGTCATAGAACATCATGAGAGACCTGGA 200
|||||
1  LysGluAsnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAAATGCAGACAGCAGCTGAGCTTCGAGAGATTCAATCATGCTGATGG 250
|||||
17 pThrAsnAlaAspLysGlnLeuSerPheGluGlnPheIleMetLeuMetA 34
251 CGAGGCTTAACCTGGGCTCCACGAGAGATGCACGAGGGTGACGAGGGC 300
|||||
34 IaArgLeuThrTyrPalaSerHisGluLysMetHisGluGlnLysAspGluGly 50
301 CCGGGCCACACCATTAAGCAGGCTCGGGGAGGAGGACCCCC 342
|||||
51 ProGluHisHisHisLysProGlyLeuGlyGluGlyThrPro 64
```

seq_name: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT: AAM20352

seq_documentation_block:

ID AAM20352 standard; Protein; 64 AA.

AC AAM20352;

DT 12-OCT-2001 (first entry)

DE Peptide #6786 encoded by probe for measuring cervical gene expression.

KW Probe; human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer.

OS Homo sapiens.

PN WO200157278-A2.

XX 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US00670.

PF 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human cervical epithelial cells -

XX Claim 27; SEQ ID No 25178; 487bp; English.
PS The present invention relates to human single exon nucleic acid probes
XX (SENP: see AAI10068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 64 AA;

alignment_scores:
Quality: 351.00 Length: 64
Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382A-2 x AAM20352 ..
Align seg 1/1 to: AAM20352 from: 1 to: 64

151 AAGGAGATAGATGAAAGGTCATAGACATCATGAGGAGCTGGA 200
|||||
1 LysGluAsnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAAATGCAGACAAAGCAGCTGAGCTTCGAGAGTTTCATCATGCTGATGG 250
|||||
17 pThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetA 34
251 CGAGGCTAACCTGGGCTCCCGACGAGAAGATGCACGAGGCTGACGAGGC 300
|||||
34 IaArgLeuThrTrpAlaSerHisGlnLysMetHisGlnLysAspGluGly 50
301 CCTGGCCACACCATTAAGCCAGGCTCGGGAGGAGGCCACCC 342
|||||
51 ProGlyHisHisHisLysProGlyLeuGlyGluGlyThrPro 64

seq_name: /SIDSI/gcgdata/hold_geneseq/geneseq-emb1/AA2001.DAT:AAM34703
seq_documentation_block:
ID AAM34703 standard; Protein: 64 AA.
XX
AC AAM34703;
XX
XX 17-OCT-2001 (first entry)
XX
DE Peptide #8740 encoded by probe for measuring placental gene expression.
XX
KW Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
XX Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001MO-US00663.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-48897/53.
XX
DR
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
PT
XX
PS Claim 27; SEQ ID No 34972; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI3315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
SQ Sequence 64 AA;

alignment_scores:
Quality: 351.00 Length: 64
Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382A-2 x AAM34703 ..
Align seg 1/1 to: AAM34703 from: 1 to: 64

151 AAGGAGATAGATGAAAGGTCATAGACATCATGAGGAGCTGGA 200
|||||
1 LysGluAsnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAAATGCAGACAAAGCAGCTGAGCTTCGAGAGTTTCATCATGCTGATGG 250
|||||
17 pThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetA 34
251 CGAGGCTAACCTGGGCTCCCGACGAGAAGATGCACGAGGCTGACGAGGC 300
|||||
34 IaArgLeuThrTrpAlaSerHisGlnLysMetHisGlnLysAspGluGly 50
301 CCTGGCCACACCATTAAGCCAGGCTCGGGAGGAGGCCACCC 342
|||||
51 ProGlyHisHisHisLysProGlyLeuGlyGluGlyThrPro 64

seq_name: /SIDSI/gcgdata/hold_geneseq/geneseq-emb1/AA2001.DAT:ABB44612
seq_documentation_block:
ID ABB44612 standard; Protein: 113 AA.
XX
AC ABB44612;
XX
XX 25-JAN-2002 (first entry)
XX
DE Mouse wound healing related polypeptide SEQ ID NO 101.
XX
KW Human; mouse; vulnery; dermatological; skin disorder; wound healing;
KW gene therapy.
XX
XX Mus musculus.
XX
PN CA2325226-A1.
XX
PD 17-MAY-2001.
XX
XX 16-NOV-2000; 2000CA-2325226.
PR 17-NOV-1999; 99DE-1055349.
PR 17-DEC-1999; 99US-0172511.
PR 20-JUN-2000; 2000DE-1030149.

XX (SWIT-) SWITCH BIOTECH AG.
 XX Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;
 XX MPI, 2001-433142/47.
 XX
 XX Use of novel polypeptide or its variant or nucleic acid encoding the
 XX polypeptide for diagnosing and/or preventing and/or treating skin
 XX disorders and/or treatment in wound healing or for identifying active
 XX substances -
 XX
 XX Claim 3; Page 245; 265pp; English.
 XX
 XX The invention relates to the use of a polypeptide (ABBA4544-ABBA4601,
 XX ABBA4606-ABBA4623) or its variant or encoding nucleic acid
 XX (ABA81990-ABA81995, ABA82016-ABA82032) with vulnerary and/or
 XX dermatological activity for the diagnosis, prevention and treatment of
 XX skin disorders and treatment in wound healing or for the identification
 XX of pharmacologically active substances. The nucleic acids are useful in
 XX gene therapy.
 XX Note: The printed sequence listing for this specification was incomplete,
 XX terminating part way through SEQ ID NO 106. The remaining data was
 XX obtained from EPO data for an equivalent patent (EP1114862).
 XX
 XX Sequence 113 AA;

alignment_scores: Quality: 329.50 Length: 107
 Ratio: 3.702 Gaps: 1
 Percent Similarity: 83.178 Percent Identity: 59.813

alignment_block:

US-09-806-382A-2 x ABBA4612 ..

Align seg 1/1 to: ABBA4612 from: 1 to: 113

```

16 TCGAGAGTGGAAAGCAACATAGACATCATCAACACCTTCACCAATA 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 SerGlnMetGluArgSerIleThrIleIleAspThrPheHisGlnI 23
66 CUCGTGGAAGCTGGGGACCCAGACACCTGACACGGGGGAATCAAG 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
23 rSerArgLysGluGlyHisProAspThrLeuSerLysGluPheArg 40
116 ACCTGTCGCAAAAGATCTGCAAAATTTCTCAGAGAGAGATAGAAT 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
40 lMetValGluValGlnLeuAlaThrPheMetLysGluLysArgGln 56
166 GAAAGGTCATAGAACACATCATGAGAGACTGACACAAATGACAGCA 215
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
57 GluAlaLeuIleAsnAspIleMetGluAspThrAsnGlnAspAs 73
216 GAGCGTGAAGCTTCGAGAGAGTTCATCATGCTGAGGAGCTAACCTGG 265
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
73 ngInLeuSerPheGluGluCysMetMetLeuAlaLysLeuIlePhe 90
266 CCTCCACGAGAAATGACAGAGGTTGAC...GAGGACCTGAGCCACAC 312
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
90 lAcylHisGluLysLeuHisGluAsnAsnProArgGlyHisLysHis 106
313 CATTAAGCCAGGCTCGGGAG 333
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
107 HisGlyLysGlyCysGlyLys 113

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seq_name: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAU30604

seq_documentation_block:

ID AAU30604 standard; Protein: 153 AA.

XX AC AAU30604;

XX

DT 18-DEC-2001 (first entry)
 XX
 XX Novel human secreted protein #1095.
 DE
 XX
 XX Human: vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200179449-A2.
 PN
 XX
 XX 25-OCT-2001.
 PD
 XX
 XX 16-APR-2001; 2001WO-US08656.
 PF
 XX
 XX 18-APR-2000; 2000US-0552929.
 PR
 XX 26-JAN-2001; 2001US-0770160.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX
 XX MPI, 2001-611725/70.
 DR
 XX
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 XX vaccination, testing and therapy -
 PT
 XX
 XX
 XX
 XX Claim 20; Page 317; 765pp; English.
 PS
 XX
 XX The invention relates to novel human secreted polypeptides. The
 XX polypeptides and antibodies to the polypeptides are useful for
 XX determining the presence of or predisposition to a disease associated
 XX with altered levels of polypeptide. The polypeptides are also useful for
 XX identifying agents (agonists and antagonists) that bind to them. Cells
 XX expressing the proteins are useful for identifying a therapeutic agent
 XX for use in treatment of a pathology related to aberrant expression or
 XX physiological interactions of the polypeptide. Vectors comprising
 XX the nucleic acids encoding the polypeptides and cells genetically
 XX engineered to express them are also useful for producing the proteins.
 XX The proteins are useful in genetic vaccination, testing and
 XX therapy, and can be used as nutritional supplements. They may be used to
 XX increase stem cell proliferation; to regulate haematopoiesis; and in
 XX bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 XX CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 XX CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 XX sequences of novel human secreted proteins of the invention.
 SO
 XX Sequence 153 AA;

alignment_scores: Quality: 315.50 Length: 122
 Ratio: 3.286 Gaps: 7
 Percent Similarity: 78.689 Percent Identity: 63.115

alignment_block:

US-09-806-382A-2 x AAU30604 ..

Align seg 1/1 to: AAU30604 from: 1 to: 153

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1 ATGACTTGCAAAATGTCGCAG...CTGGAACGCACATCATGACCATCAT 47
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
32 MetThrCysGlyMetProGlnHisValThrGlnGln**ArgProIle 48
48 CAACACCTTCACCAATATCTGTGAGAGCTGGGGACCCAGACACCTGA 97
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
48 eAsnThrSerHisGlnIleValLysLeuGlyHisProAspThrIleu 65
98 ACCAGGGGGAATTCAAAGAGCTGGTGGCAAAAGATCTGCAAAATTTTCTC 147
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 sngInGlyGluPheLysGluLeuValArgLysAspLeuGlnAsnPheLeu 81

```

```
148 AAGAGGAGATATAGATGAAAAGTCATAGAACATCATGAGGAGCCT 197
|||||
82 LysLysGlnAsnLysAsnGlnLysValIleGlnHisIleMetArgGlyPr 98
|||||
198 GGACACA...AATGCAGACAAG.....CAGCTGAGCTTCGAGGAGTCA 238
|||||
98 oGlyThrGlnAsnAlaGlnProAlaGlnLeuSer...ArgGlnPheI 114
|||||
239 TCATGCTGATGGGAGGCTACCTGGGCGCTCC.....CAGCGAGGATG 282
|||||
114 IeMetLeuMetGlyGlnAla***ProGlyAlaPheProArgGlyTyrIle 130
|||||
283 CAGCAGGAGT...GACGAGGCGCCCTGGCCACACCATATAG...CCAGGCGCT 326
|||||
131 AlaArgGlyLeuThrGlnGlyProGlnHisProAsnLys***ProGlyPr 147
|||||
327 CGGGGAGGCGCACCCCC 342
|||||
147 oGlyGlyGlyAlaPro 152

seq_name: /SIDSL/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:AAU29794
seq_documentation_block:
ID AAU29794 standard; Protein; 57 AA.
XX
AC AAU29794:
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #285.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HXSE-) HXSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX
PS Claim 20; Page 195; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
```

```
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 57 AA.

alignment_scores:
    Quality: 267.00      length: 56
    Ratio: 4.944
    Percent Similarity: 96.429      Percent Identity: 85.714

alignment_block:
US-09-806-382A-2/rev x AAU29794
Align seg 1/1 to: AAU29794 from: 1 to: 57

188 ATGATGTGTTCTATGACCTTTTCATCTTATTCCTCTTGAGAAAT 139
|||||
1 MetMetCysSerMetThrLeuSerPheIlePheSerPheMetArgLysIle 17
|||||
138 TTGCAGATCTTTTCGACCCAGCTCTTGAATTCCTGGTGGAGGTG 89
|||||
17 ucysArgSerIleArgAlaSerSerTrpAsnSerProTrpPheArgValS 34
|||||
88 CTGGGTGCCCCAGCTTCACAGAGTATTGTGGAAGGTGTGATGATGCTC 39
|||||
34 exGlyCysProSerPheThrGlnGlyTrpTrpLysValIleMetMetVal 50
|||||
38 TCTATGTTGCGTTCCAGC 21
|||||
51 TyrMetLeuArgSerSer 56

seq_name: /SIDSL/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:ABB42295
seq_documentation_block:
ID ABB42295 standard; Peptide; 44 AA.
XX
AC ABB42295:
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #9801 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analysing gene expression in human fetal liver -
XX
PS Claim 27; SEQ ID NO 34930; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
```

CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 44 AA;

alignment_scores:

Quality: 229.00 Length: 44
Ratio: 5.205 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-2 x ABB42295 ..

Align seg 1/1 to: ABB42295 from: 1 to: 44

19 CAGCTGAACGCAACATAGAGACCATCATCAACACCTTCACCAATACTC 68
|||||
1 GlnleuGluaRgAsnIleGluThrIleLeuSnrhrPheHisGlnTyse 17
69 TGTGAAGCTGGGGCACCAGACCCCTGAACCGGGGGAATTCAAGAGC 118
|||||
17 TVallylsleuGlyHisProAspThrLeuAsnGlnGlyIuphelysGluL 34
119 TGTGCGCAAGAAGATCTGCAAAATTTCTCAAG 150
|||||
34 euValaRgLyAspLeuGlnAsnPheLeuLys 44

seq_name: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:ABB25798

seq_documentation_block:

ID ABB25798 standard; Protein: 44 AA.

XX AC ABB25798;

XX DT 23-JAN-2002 (first entry)

XX DE Protein #7797 encoded by probe for measuring heart cell gene expression.

XX KW Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

XX OS Homo sapiens.

XX PN WO200157274-A2.

XX PD 09-AUG-2001.

XX PE 30-JAN-2001; 2001WO-US00666.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488899/53.

XX PT Single exon nucleic acid probes for analyzing gene expression in human

PS Claim 15; SEQ ID No 27568; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 44 AA;

alignment_scores:

Quality: 229.00 Length: 44
Ratio: 5.205 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-2 x ABB25798 ..

Align seg 1/1 to: ABB25798 from: 1 to: 44

19 CAGCTGAACGCAACATAGAGACCATCATCAACACCTTCACCAATACTC 68
|||||
1 GlnleuGluaRgAsnIleGluThrIleLeuSnrhrPheHisGlnTyse 17
69 TGTGAAGCTGGGGCACCAGACCCCTGAACCGGGGGAATTCAAGAGC 118
|||||
17 TVallylsleuGlyHisProAspThrLeuAsnGlnGlyIuphelysGluL 34
119 TGTGCGCAAGAAGATCTGCAAAATTTCTCAAG 150
|||||
34 euValaRgLyAspLeuGlnAsnPheLeuLys 44

seq_name: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:AAM63181

seq_documentation_block:

ID AAM63181 standard; Protein: 44 AA.

XX AC AAM63181;

XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35286.

XX KW Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.

XX OS Homo sapiens.

XX PN WO200157275-A2.

XX PD 09-AUG-2001.

XX PE 30-JAN-2001; 2001WO-US00667.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX

PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -

XX
PS Example 4; SEQ ID NO: 35286; 650pp + Sequence Listing; English.
XX

CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.

XX
SQ Sequence 44 AA;

alignment_scores:
Quality: 229.00 Length: 44
Ratio: 5.205 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382A-2 x AAM63181 ..

Align seg 1/1 to: AAM63181 from: 1 to: 44

```
19 CAGCTGGAACGCACATAGAGACATCATCAACACCTTCACCAATACTC 68
|||||
1 GlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTyrse 17
69 TGTGAAGCTGGGGCACCCAGACACCTTGACACGGGGGATTCAAAGAGC 118
|||||
17 rVallysLeuGlyHisProAspThrLeuAsnGlnGlyIuPheLysGluL 34
119 TGGTGCAGAAAGATCTGCAGAAATTTCTCAAG 150
|||||
34 euValArgLysAspLeuGlnAsnPheLeuLys 44
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OM of: US-09-806-382a-2 to: Pending_Patents_AA_Main:* out_format : pfs
 Date: Sep 9, 2002 3:22 PM

About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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 -GAPOP=12.000 -GAPEXT=4.000 -MINMAP=0.100 -LOOPEL=0.000
 -LOOPEXT=0.000 -GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000
 -XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
 -YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
 -MATRIX=bloms62 -TRANS=human40.cdi -LIST=45 -DOCLIGN=200
 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pts -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USBR=US09806382.4CGN1.1571 -NCPU=6 -ICPU=3 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPPY -WAIT -THREADS=1

Search information block:

Query: US-09-806-382a-2
 Query length: 345
 Database: Pending_Patents_AA_Main:*
 Database sequences: 3502263
 Database length: 351980561
 Search time (sec): 409.890000

score list:

Sequence	Strd Orig	ZScore	Escore	len	Documentation
/cgn2.6/ptodata/2/paa/PCYUS.COMB.pep:US-09-806-7634		448.00	808.16	1.3e-36	18
/cgn2.6/ptodata/2/paa/US094.COMB.pep:US-09-488-725A-6711		417.00	755.97	1.6e-33	11
/cgn2.6/ptodata/2/paa/PCYUS.COMB.pep:US-09-806-7634		371.00	666.54	8.5e-29	21
/cgn2.6/ptodata/2/paa/US087.COMB.pep:US-08-759-913-7		335.50	644.06	2.8e-27	113
/cgn2.6/ptodata/2/paa/US092.COMB.pep:US-09-205-680-7		335.50	644.06	2.8e-27	113
/cgn2.6/ptodata/2/paa/US094.COMB.pep:US-09-492-026-7		335.50	644.06	2.8e-27	113
/cgn2.6/ptodata/2/paa/PCYUS.COMB.pep:US-09-864-761-40349		351.00	641.09	7.3e-27	64
/cgn2.6/ptodata/2/paa/US098.COMB.pep:US-09-714-593-101		329.50	596.71	1.2e-24	113
/cgn2.6/ptodata/2/paa/US097.COMB.pep:US-09-714-593-101		329.50	596.71	1.2e-24	113
/cgn2.6/ptodata/2/paa/US060.COMB.pep:US-60-340-187-1029		320.00	579.58	1.1e-23	111
/cgn2.6/ptodata/2/paa/US060.COMB.pep:US-60-340-187-1030		320.00	579.58	1.1e-23	111
/cgn2.6/ptodata/2/paa/US060.COMB.pep:US-60-340-187-1031		320.00	579.58	1.1e-23	111
/cgn2.6/ptodata/2/paa/PCYUS.COMB.pep:US-09-834-366-20109		315.50	568.43	3.4e-23	115
/cgn2.6/ptodata/2/paa/PCYUS.COMB.pep:US-09-834-366-20109		289.00	530.10	1.4e-20	52
/cgn2.6/ptodata/2/paa/US060.COMB.pep:US-60-197-873-20109		289.00	530.10	1.4e-20	52
/cgn2.6/ptodata/2/paa/PCYUS.COMB.pep:US-09-806-7634		267.00	489.36	2.4e-18	56
/cgn2.6/ptodata/2/paa/PCYUS.COMB.pep:US-09-806-7634		229.00	422.38	1.6e-14	4

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seq_documentation_block:

; Sequence 7634, Application PC/TUS0108656
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OR INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 2172-066
 ; CURRENT APPLICATION NUMBER: PCT/US01/08656
 ; CURRENT FILING DATE: 2001-04-16
 ; PRIOR APPLICATION NUMBER: 09/522,929
 ; PRIOR FILING DATE: 2000-04-18
 ; PRIOR APPLICATION NUMBER: 09/770,160
 ; PRIOR FILING DATE: 2001-01-26
 ; NUMBER OF SEQ ID NOS: 10994
 ; SOFTWARE: Custom
 ; SEQ ID NO 7634
 ; LENGTH: 181
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOMAIN

LOCATION: (6)..(43)
 ; OTHER INFORMATION: S-100/ICABP type calcium binding protein domain identified by
 ; OTHER INFORMATION: EMATRIX, accession number BL00303A, p-value=6.667e-26, raw sco
 ; OTHER INFORMATION: of 21.77
 ; NAME/KEY: DOMAIN
 ; LOCATION: (7)..(55)
 ; OTHER INFORMATION: S-100/ICABP type calcium binding domain identified by Pfam,
 ; OTHER INFORMATION: accession name S_100, E-value=2e-08, Pfam score of 41.4
 PCT-US01-08656-7634

alignment_scores:

Quality	Length
Ratio: 4.480	114
Percent Similarity: 87.719	Gaps: 3
Percent Identity: 82.456	

alignment_block:

US-09-806-382a-2 x PCT-US01-08656-7634 ..

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13	ATGTCGACGCTGAGACGACATGACATCATCATCAACCTTCCACCA	62
4	MetrpGlnLeuGluArgAsnIleGluThrIleIleLsnThrPheHsGl	20
63	ATACTGTGAGCTGGGGCACCACACCTTGACACGGGGAATCA	112
20	ntYserValIysLeuGlyHisProAspThrLeuAsnGlnGlyIubHel	37
113	AAGAGCTGCTGCGAAAGATCTG...CAAAATTTCTCAGAGAGAAAT	159
37	YsgIleuValArgLysAspLeuGlyGlnAsnPheLeuLysGlnAsn	53
160	AAGATGAAGAGTCATGACATGACATCATGAGGAGCTGACACAAATGC	209
54	LysAsnGlnLysValIleGlnHisIleHisLysLysLysLysLysLys	70
210	AGACAAGAGCTGAGCTGAGAGAGTTTCATGCTGATGGCGAGCTAA	259
70	aAlaGlnIleuSerPheGlnGluPheIleMetLeuMetLysAlaL	87
260	CCTGGGCTGC.....CAGCAAGATGACGAGGAGGAGGAGGCT	303
87	YspProGlyAlaLeuProThrArgMetHisGlyAspLysGlyPro	103
304	GGCCACCAACCATMACCAGGCTCGGGGAGGAGGACCC	342
104	TrpProProHisLysProGlyLeuGlyGlyThrPro	117

seq_name: /cgn2.6/ptodata/2/paa/US094.COMB.pep:US-09-488-725A-6711

seq_documentation_block:

; Sequence 6711, Application US/09488725A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
 ; FILE REFERENCE: 784FLPCT
 ; CURRENT APPLICATION NUMBER: US/09/488,725A
 ; CURRENT FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US-09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: US09/598,042
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: US09/620,312
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: US09/653,450
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: US09/662,191
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: US09/693,036
 ; PRIOR FILING DATE: 2000-10-19

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;; PRIOR APPLICATION NUMBER: US09/727,344
;; PRIOR FILING DATE: 2000-11-29
;; NUMBER OF SEQ ID NOS: 7144
;; SOFTWARE: PL_FL_genes_b Versions 1.0
;; SEQ ID NO 6711
;; LENGTH: 114
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(114)
;; OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-6711
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alignment_scores:
  Quality: 417.00      Length: 108
  Ratio: 4.299         Gaps: 0
  Percent Similarity: 89.815   Percent Identity: 71.296
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alignment_block:
US-09-806-382A-2 x US-09-488-725A-6711 ..
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1 ATGACTTGCAAAATGTCGACGTGAGACGCAACATAGAGACCATCATCA 50
  ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7 MetThrCysLysMetSerGlnLeuGlnArgAsnIle**ThrMetIleAs 23
51 CACCTTCACCAATACCTGTGAGACGTGGGACCCAGACACCTGGAACC 100
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 nThrLeuHisHisTyrSerValLysLeuGlnHisProAspHisLeu 40
101 AGGGGGAATTCAAAGAGCTGTGCAAAAAGATCTGCAAAATTTCTCAAG 150
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
40 IsGlyGlnPheLysGlnLeuValArgThrAspLeuHisAsnIleLeuMet 56
151 AAGGGAATAGAAATGAAAGCTATAGACACATCATGAGAGACTGGA 200
  ||||||| |||:|||||:|||||:|||||:|||||:|||||:|||||
57 LysGlnAsnLysAsnAspGlnIleIle**HisIleMetGlnAspLeuAs 73
201 CACAATATCAGACAGACAGCTGAGCTTCAGAGATTCATCATGCTGATGG 250
  ||||||| |||:|||||:|||||:|||||:|||||:|||||:|||||
73 PThrAsnIleHisMetGlnIleIlePheLysGlnLeuIleMetLeuMet 90
251 CGAGGCTTACCTGGCCCTCCACAGAGAAGATGACAGAGGTGACGAGGC 300
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
90 IamLeuIleThrTyrSerTyrHisAspAsnMetHisAspAlaAspTyrGly 106
301 CCTGGCCACGACCATACGACGAGC 324
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
107 ProGlyGlnGlnHisArgProGly 114
```

seq_name: /cgn2_6/plodata/2/paa/PCTUS_COMB.pep:PCT-US01-08656-5822

```
seq_documentation_block:
;; Sequence 5822, Application PC/TUS0108656
;; GENERAL INFORMATION:
;; APPLICANT: HySeq, Inc
;; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
;; FILE REFERENCE: 21272-066
;; CURRENT APPLICATION NUMBER: PCT/US01/08656
;; PRIOR FILING DATE: 2001-04-16
;; PRIOR APPLICATION NUMBER: 09/522,929
;; PRIOR FILING DATE: 2000-04-18
;; PRIOR APPLICATION NUMBER: 09/770,160
;; NUMBER OF SEQ ID NOS: 10994
;; SOFTWARE: Custom
;; SEQ ID NO 5822
;; LENGTH: 211
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
```

```
;; NAME/KEY: DOMAIN
;; LOCATION: (87)...(124)
;; OTHER INFORMATION: S-100/ICaBP type calcium binding protein domain identified by
;; OTHER INFORMATION: EMBL, accession number B100303B, p-value=2.698e-13, raw sco
;; OTHER INFORMATION: of 26.15
;; NAME/KEY: DOMAIN
;; LOCATION: (36)...(85)
;; OTHER INFORMATION: S-100/ICaBP type calcium binding domain identified by Pfam,
;; OTHER INFORMATION: accession name S_100, E-value=0.094, Pfam score of 7.3
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(211)
;; OTHER INFORMATION: Xaa = x or * as defined in Table 2
PCT-US01-08656-5822
```

```
alignment_scores:
  Quality: 371.00      Length: 120
  Ratio: 3.747         Gaps: 5
  Percent Similarity: 82.500   Percent Identity: 68.333
```

```
alignment_block:
US-09-806-382A-2 x PCT-US01-08656-5822 ..
```

Align seg 1/1 to: PCT-US01-08656-5822 from: 1 to: 211

```
1 ATGACTTGCAAAATGTCGACG...CTGGAACGCAACATAGAGACCATCAT 47
  ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
32 MetThrCysGlyMetProGlnHisValThrGlnIle**ArgProIleIle 48
48 CAAACCTTCACCAATACCTGTGTAAGCTGGGACCCA...GACACCC 94
  ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48 eAsnThrSerHisGlnTyrSerValLysLeuGlnHisProArgHisProG 65
95 TGACACGAGGGGAATTCAAAGAGCTGTGCGAAAGATGTGCAAAATTT 144
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 LurThrArgGlyArgPheLysGlnLeuValArgLysAspLeuIleAsnPro 81
145 CTCGAAGAAGAGAAATAGAAATGAAAGCTCATAGACACATCATGAGAGA 194
  ||||||| |||:|||||:|||||:|||||:|||||:|||||:|||||
82 LeuLysLysGlnAsnLysAsnGlnLysValIleGlnHisIleMetGlnAs 98
195 CCTGACACCAATATGACAGACACAGCTGAGCTTC...GAGGAGTTTCATCA 241
  ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
98 PLeuAspThrAsnAlaAspLysGlnLeuSerPheArgGlnGluPheIle 115
242 TGCTGATGGCGAGGCTTAACCTGGGCTCC...CAGGAGAAGATGGCC 285
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
115 eLeuMetGlyGlnIleIle**ProGlyAlaIlePheProArgArgLysIleAla 131
286 GAGGCT...GACGAGGGCCCTGGCCACCAACCATTAAGCAGGCTCGGGGA 332
  :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
132 ArgGlyLeuThrGlnGlyProGlyHisHisLysProGlyProGlyGly 148
333 GGGCACCCCC 342
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
148 yGlyAlaPro 151
```

seq_name: /cgn2_6/plodata/2/paa/US087_COMB.pep:US-08-759-913-7

```
seq_documentation_block:
;; Sequence 7, Application US/08759913
;; GENERAL INFORMATION:
;; APPLICANT: Bandmen, Olga
;; APPLICANT: Goli, Surya K.
;; APPLICANT: Hillman, Jennifer L.
;; TITLE OF INVENTION: NOVEL HUMAN S100 PROTEINS
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: US
```

```
ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,913
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0172 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 478287
;
; US-08-759-913-7
```

```
alignment_scores:
    Quality: 355.50      Length: 107
    Ratio: 3.864        Gaps: 1
    Percent Similarity: 85.981    Percent Identity: 64.486
```

alignment_block:
US-09-806-382A-2 x US-08-759-913-7 ..

Align seg 1/1 to: US-08-759-913-7 from: 1 to: 113

```
16 TCGCAGCTGGAGCGACATAGACACCATCATACACCTTCACCAATA 65
|||||
7 SerGlnLeuGluArgSerIleSerThrIleIleAsnValPheHisGlnTy 23
66 CTCTGTGAAGCTGGGCGACCCAGACACCCCTGAACCGGGGAATTCAAG 115
|||||
23 rSerArgLysTyrGlnHisProAspThrLeuAsnLysAlaGluPheLysG 40
116 AGCTGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGAGATAAGAT 165
|||||
40 lMetValAsnLysAspLeuProAsnPheLeuLysArgGluLysArgAsn 56
166 GAAAAGGTCAATAGACACATCATGAGAGACCTGGACAAATTCAGACA 215
|||||
57 GluAsnLeuLeuArgAspIleMetGluAspLeuAspThrAsnGlnAspAs 73
216 GCAGCTGAGCTTGCAGAGATTCATCATGCTGATGGCGAGGCTTAACCTG 265
|||||
73 nGlnLeuSerPheGluGluLysMetLeuMetGlyLysLeuIlePheAsn 90
266 CTCTCCGACGAAAGATGACAGAGGTGACAGAGGCCCTGCGCCACACCAT 315
|||||
90 lAcysHisGlnLysLeuHisGlnAsnAsnPro...ArgGlnHisAspHis 105
316 AAGCCAGGCTCGGGAGGAGGC 336
|||
106 ArgHisGlyLysGlyCysGly 112
```

seq_name: /cgn2_6/ptodata/2/paa/US092_COMP.pep:US-09-205-680-7
seq_documentation_block:

```
; Sequence 7, Application US/09205680
;
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN S100 PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
;
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,680
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/918,727
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0373 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 488157
;
; US-09-205-680-7
```

```
alignment_scores:
    Quality: 355.50      Length: 107
    Ratio: 3.864        Gaps: 1
    Percent Similarity: 85.981    Percent Identity: 64.486
```

alignment_block:
US-09-806-382A-2 x US-09-205-680-7 ..

Align seg 1/1 to: US-09-205-680-7 from: 1 to: 113

```
16 TCGCAGCTGGAAGCGACATAGAGACATCATCAACACCTTCACCAATA 65
|||||
7 SerGlnLeuGluArgSerIleSerThrIleIleAsnValPheHisGlnTy 23
66 CTCTGTGAAGCTGGGCGACCCAGACACCCCTGAACCGGGGAATTCAAG 115
|||||
23 rSerArgLysTyrGlnHisProAspThrLeuAsnLysAlaGluPheLysG 40
116 AGCTGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGAGATAAGAT 165
|||||
40 lMetValAsnLysAspLeuProAsnPheLeuLysArgGluLysArgAsn 56
166 GAAAAGGTCAATAGACACATCATGAGAGACCTGGACAAATTCAGACA 215
|||||
57 GluAsnLeuLeuArgAspIleMetGluAspLeuAspThrAsnGlnAspAs 73
```

```

216 GCAGCTGACCTTCGAGAGTTCATGCTGATGCGAGGCTAACCTGGG 265
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
73 nglnleuserpneglucLucysmetleuMetglyLysleuIlePhea 90
266 CCTCCACAGAGAAGATGACAGAGGCTGACGAGGCCCTGGCCACACCAT 315
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
90 lacyshtsglulysleuHtsgluasnAhnPro...ArgglyHtshsPhis 105
316 AAGCCAGCGCTCGGGGAGGCG 336
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
106 ArgHtsglyLysglyCysgly 112

seq_name: /cgn2_6/ptodata/2/paa/US094_COMB.pep:US-09-492-026-7

seq_documentation_block:
: Sequence 7, Application US/09492026A
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: Bandman, Olga
: Corley, Neil C.
: Lal, Preeti
: Shah, Purvi
: TITLE OF INVENTION: HUMAN S100 PROTEINS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/492.026A
: FILING DATE: 26-Jan-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: <Unknown>
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Colette C. Muenzen
: REGISTRATION NUMBER: 39,784
: REFERENCE/DOCKET NUMBER: PF-0373 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 113 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: Genbank
: CLONE: 488157
: SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-492-026-7

alignment_scores:
Quality: 355.50 Length: 107
Ratio: 3.864 Gaps: 1
Percent Similarity: 85.981 Percent Identity: 64.486

alignment_block:
US-09-806-382A-2 x US-09-492-026-7

```

```

Align seq 1/1 to: US-09-492-026-7 from: 1 to: 113

16 TCCACAGCTGAGACGCAACATAGACACCATCATCAACACCTTCCACCAATA 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
7 SerGlnleucluarGysSerIleSerThrIleIleasnValPhehtsgInty 23
66 CTCTGTGAGCTGGGACCCACGACACCCGTGACGAGCGGGGGGATTCGAAG 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
23 tSerArgLysTyrglyHtshsPhisPtnleuasnLysAlaGlnPheLysG 40
116 AGCTGTGCGAAGATCTGCAAAATTTCTCAAGAGAGGAATTAAGAT 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
40 lueValasnLysAspLeuProAsnPhelenuLysArgGluLysArgAsn 56
166 GAAAGGTATAGACACATCATGAGAGACCTTGACACAAATTCACAA 215
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
57 GluAsnleuLuarGAspIleMetGluAspLeuAspThrAsnLnsAsps 73
216 GCAGCTGACCTTCGAGAGTTCATGCTGATGCGAGGCTAACCTGGG 265
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
73 nglnleuserpneglucLucysmetleuMetglyLysleuIlePhea 90
266 CCTCCACAGAGAAGATGACAGAGGCTGACGAGGCCCTGGCCACACCAT 315
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
90 lacyshtsglulysleuHtsgluasnAhnPro...ArgglyHtshsPhis 105
316 AAGCCAGCGCTCGGGGAGGCG 336
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
106 ArgHtsglyLysglyCysgly 112

seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-00663-34972

seq_documentation_block:
: Sequence 34972, Application PC/TUS0100663
: GENERAL INFORMATION:
: APPLICANT: Molecular Dynamics, Inc.
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
: FILE REFERENCE: PB 0004 WO 7
: CURRENT APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 04 February 2000 (04.02.00)
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 26 May 2000 (26.05.00)
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 03 August 2000 (03.08.00)
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 03 October 2000 (03.10.00)
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 27 September 2000 (27.09.00)
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 21 September 2000 (21.09.00)
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 30 June 2000 (30.06.00)
: NUMBER OF SEQ ID NOS: 38837
: SOFTWARE: Molecular Dynamics Sequence Listing Engine
: SEQ ID NO 34972
: LENGTH: 64
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC011666.18
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
: OTHER INFORMATION: SWISSPROT HIT: P06702, EVALUE 2.00e-34
: OTHER INFORMATION: EST_HUMAN HIT: AT720432.1, EVALUE 2.00e-33
PCT-US01-00663-34972

```

alignment_scores: Length: 64
 Quality: 351.00 Gaps: 0
 Ratio: 5.484
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382a-2 x PCT-US01-00663-34972 ..

Align seg 1/1 to: PCT-US01-00663-34972 from: 1 to: 64

```

151 AAGGAGATTAAGATGAAGAGTGCATAGACATCATGAGAGCTGGA 200
    |||||||
1  LysGluAsnLysAsnGlnLysValIleGlnHisIleMetGluAspLeuAs 17
201 CCAATGTCAGACAGACAGCTGAGTTCGAGAGTTCATCATGCTGATGG 250
    |||||||
17 phtAsnAlaAspLysGlnLeuSerPheGlnIuPheIleMetLeuMetA 34
251 CGAGGCTAACCTGGGCTCCAGAGAGATGCACGAGGGTGACGAGGCG 300
    |||||||
34 laArgLeuThrTrpAlaSerHisGlnLysMetHisGlnLysAspGlnGly 50
301 CCGGCCACACCATTAAGCCAGGCTCGGGAGGACCCCC 342
    |||||||
51 ProGlnHisHisHisLysProGlnLysGlnGlyThrPro 64

```

seq_name: /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-864-761-40349

seq_documentation_block:

```

; Sequence 40349, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408

```

```

; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40349
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```

```

; OTHER INFORMATION: MAP TO AC011666.18
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1e+02
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.2
; OTHER INFORMATION: SWISSPROT HIT: P06702, EVALUATE 2.00e-34
; OTHER INFORMATION: EST_HUMAN HIT: A1720432.1, EVALUATE 2.00e-33
; US-09-864-761-40349

```

alignment_scores: Length: 64
 Quality: 351.00 Gaps: 0
 Ratio: 5.484
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382a-2 x US-09-864-761-40349 ..

Align seg 1/1 to: US-09-864-761-40349 from: 1 to: 64

```

151 AAGGAGATTAAGATGAAGAGTGCATAGACATCATGAGAGCTGGA 200
    |||||||
1  LysGluAsnLysAsnGlnLysValIleGlnHisIleMetGluAspLeuAs 17
201 CCAATGTCAGACAGACAGCTGAGTTCGAGAGTTCATCATGCTGATGG 250
    |||||||
17 phtAsnAlaAspLysGlnLeuSerPheGlnIuPheIleMetLeuMetA 34
251 CGAGGCTAACCTGGGCTCCAGAGAGATGCACGAGGGTGACGAGGCG 300
    |||||||
34 laArgLeuThrTrpAlaSerHisGlnLysMetHisGlnLysAspGlnGly 50
301 CCGGCCACACCATTAAGCCAGGCTCGGGAGGACCCCC 342
    |||||||
51 ProGlnHisHisHisLysProGlnLysGlnGlyThrPro 64

```

seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-714-593-101

seq_documentation_block:

```

; Sequence 101, Application US/09714593
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorne-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of polypeptides or nucleic acids
; TITLE OF INVENTION: encoding these for the diagnosis or treatment of skin
; TITLE OF INVENTION: disorders, and their use for the identification of
; TITLE OF INVENTION: pharmacologically active substances
; FILE REFERENCE: 50125/009002
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US/09/714,593
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: DE 19955349.1-41
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: US 60/172,511
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: DE 10030149.5-41
; PRIOR FILING DATE: 2000-06-20

```

```

; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 101
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-714-593-101

```

```

alignment_scores:
  Quality: 329.50      Length: 107
  Ratio: 3.702        Gaps: 1
  Percent Similarity: 83.178  Percent Identity: 59.813

```

alignment_block:

US-09-806-382a-2 x US-09-714-593-101 ..

Align seg 1/1 to: US-09-714-593-101 from: 1 to: 113

```

16 TCGACAGCTGGAAAGCAGCATATAGACATCATACACCTTCACCAATA 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 SerGlnMetGluArgSerIleThrIleIleAspThrPheHisGlnTyr 23
66 CTTGTGGAAGCTGGGGGACCCGACACCTGACACGAGGGGGAATTCAAAG 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 rSerTrgLySGluGlyHisProAspThrLeuSerLySGluPheArgG 40
116 ACCTGGTGGAAAGATCTGCAAAATTTCTCAGAGAGAGAGATTAAGAT 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
40 lMetValGlnValGlnLeuAlaTrpMetLysLysGlnLysArgAsn 56
166 GAAAAGTCATAGAACATCATGAGAGACCTGACACAAATGACAGACAA 215
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
57 GluAlaLeuIleAsnAspIleMetGlnAspThrAsnGlnAspAs 73
216 GCAGCTGAGCTTCGAGAGTTTCATGATGCTGATGCGGAGGCTAACCTGG 265
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
73 nGlnLeuSerPheGlnGluGlyCysMetMetLeuMetAlaLysLeuIlePheA 90
266 CCTCCCGCAGAGATGACAGAGGCTGAC...GAGGGCCCTCGGCGCACAC 312
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
90 lAcYSHisGlnLysLeuHisGlnAsnAsnProArgGlyHisGlyHisSer 106
313 CATAGCCAGCGCTCGGGGAG 333
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107 HisGlyLysGlyCysGlyLys 113

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seq_name: /cgn2_6/prodata/2/paa/US60_COMB.pep:US-60-340-187-1029

seq_documentation_block:

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; Sequence 1029, Application US/60340187
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhilwei
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Meng, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 813
; CURRENT APPLICATION NUMBER: US/60/340,187
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623

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; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/04941
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/770,160
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US01/08656
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/14827
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 1192
; SOFTWARE: PL_FL_genes Version 6.0
; SEQ ID NO: 1029
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(111)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set
US-60-340-187-1029

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alignment_scores:

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  Quality: 320.00      Length: 93
  Ratio: 4.211        Gaps: 0
  Percent Similarity: 81.720  Percent Identity: 67.742

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alignment_block:

US-09-806-382a-2 x US-60-340-187-1029 ..

Align seg 1/1 to: US-60-340-187-1029 from: 1 to: 111

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19 pheSerTyrLysLeuMet**AsnThrAspPhePheLysGlyArgArgG 35
114 AGAGCTGTGCGAAGATGTCGCAAAATTTCTCAAGAGAGAGATTAAGA 163
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
35 uGlnTyrLeuValGlnLeuLeuCysAsnLeuLeuSerLysCysPhe***A 52
164 ATGAAAAGTCATAGAACATCATGAGAGACCTGACACAAATGACAGAC 213
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
52 snAspThrThrglyHisIleMetGlnAspLeuAspThrAsnAlaAsp 68
214 AAGCAGCTGAGCTTCGAGAGATTCATCATGATGAGGAGGAGGCTAACTG 263
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
69 LysGlnLeuSerPheGlnGluPheIleMetLeuMetAlaArgLeuThrTr 85

```

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264 GGCCTCCACGAGAGATGCACGAGGTGACGAGGGCCTGGCCACACCC 313
|||||
85 palaserhslglulymethisglulyspdluglyproglyhshish 102
314 ATAGCCAGGCTCGGGGAGGACCC 342
|||||
102 islysproglyleuglyglulylthp 111

seq_name: /cgn2_6/plodata/2/paa/US60_COMB.pep:US-60-340-187-1030

seq_documentation_block:
; Sequence 1030, Application US/60340187
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Weng, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 813
; CURRENT APPLICATION NUMBER: US/60/340,187
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/04941
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/770,160
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US01/08656
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/14827
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 1192
; SOFTWARE: PL_genes Version 6.0
; SEQ ID NO 1030
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; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..4(111)
; OTHER INFORMATION: Xaa - any amino acid or symbol as shown in the table 8 as set
US-60-340-187-1030

alignment_scores:
      Quality: 320.00      Length: 93
      Ratio: 4.211      Gaps: 0
Percent Similarity: 81.720      Percent Identity: 67.742

alignment_block:
US-09-806-382A-2 x US-60-340-187-1030 ..

Align seg 1/1 to: US-60-340-187-1030 from: 1 to: 111

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:::|||||
19 PheSerTylLysLeuMet**AsnThrAspPhePheLysGlyArgArgG1 35
:::|:::
114 AGAGCTGTGGCAAAAGATCTGCMAAATTCTCTCAGAGAGAGATAAGA 163
:::|:::
35 uGlnTyrLeuValGlnLeuLeuCysAsnLeuLeuSerLysCysPhe**A 52
:::|:::
164 ATGAAGAAGGTCAATAGACATCATGAGAGACCTGACACCAATGACAC 213
|:::|:::
52 snAspThrThrLglnHslMetGlnAspLeuAspThrAsnAlaAsp 68
|||||
214 AAGACGCTGAGCTTGAGAGATTCAATGCTGATGAGGAGGCTAACCTG 263
|||||
69 LysGlnLeuSerPheGlnPheLeuMetLeuMetAlaArgLeuThrTr 85
|||||
264 GGCCTCCACGAGAGATGCACGAGGTGACGAGGGCCTGGCCACACCC 313
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85 palaserhslglulymethisglulyspdluglyproglyhshish 102
314 ATAGCCAGGCTCGGGGAGGACCC 342
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102 islysproglyleuglyglulylthp 111

seq_name: /cgn2_6/plodata/2/paa/US60_COMB.pep:US-60-340-187-1031

seq_documentation_block:
; Sequence 1031, Application US/60340187
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Weng, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 813
; CURRENT APPLICATION NUMBER: US/60/340,187
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
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? PRIOR APPLICATION NUMBER: US 09/560,875
? PRIOR FILING DATE: 2000-04-27
? PRIOR APPLICATION NUMBER: PCT/US01/03800
? PRIOR FILING DATE: 2001-02-05
? PRIOR APPLICATION NUMBER: US 09/515,126
? PRIOR FILING DATE: 2000-02-28
? PRIOR APPLICATION NUMBER: US 09/577,409
? PRIOR FILING DATE: 2000-05-18
? PRIOR APPLICATION NUMBER: PCT/US01/04927
? PRIOR FILING DATE: 2001-02-26
? PRIOR APPLICATION NUMBER: US 09/519,705
? PRIOR FILING DATE: 2000-03-07
? PRIOR APPLICATION NUMBER: US 09/574,454
? PRIOR FILING DATE: 2000-05-19
? PRIOR APPLICATION NUMBER: PCT/US01/04941
? PRIOR FILING DATE: 2001-03-05
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? PRIOR FILING DATE: 2000-03-31
? PRIOR APPLICATION NUMBER: US 09/649,167
? PRIOR FILING DATE: 2000-08-23
? PRIOR APPLICATION NUMBER: PCT/US01/08631
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? PRIOR APPLICATION NUMBER: US 09/552,929
? PRIOR FILING DATE: 2000-04-18
? PRIOR APPLICATION NUMBER: US 09/770,160
? PRIOR FILING DATE: 2001-01-26
? PRIOR APPLICATION NUMBER: PCT/US01/08656
? PRIOR FILING DATE: 2001-04-18
? PRIOR APPLICATION NUMBER: US 09/577,408
? PRIOR FILING DATE: 2000-05-18
? PRIOR APPLICATION NUMBER: PCT/US01/14827
? PRIOR FILING DATE: 2001-05-16
? NUMBER OF SEQ ID NOS: 1192
? SOFTWARE: PL_FL_genes Version 6.0
? SEQ ID NO 1031
? LENGTH: 111
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(111)
? OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set for
US-60-340-187-1031
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alignment_scores:
    Quality: 320.00      Length: 93
    Ratio: 4.211        Gaps: 0
Percent Similarity: 81.720    Percent Identity: 67.742
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alignment_block:
US-09-806-382a-2 x US-60-340-187-1031 ..

Align seg 1/1 to: US-60-340-187-1031 from: 1 to: 111

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114 AGAGCTGTGCGAAGAAGATCTGCAAAATTTCTCTAGAGAAGAGAATAGA 163
   ::::: ::::: ||| ||| :::::
35 uGlnTyrLeuValGlnLeuLeuCysAsnLeuIleSerLysCysPhe**A 52
   ::::: ::::: ||| ||| :::::
164 ATGAAGAAGTCATAGACACATCATGTGAGGAGCTGCACAAATGACAGAC 213
   (:::: ::::: ||||| :::::
52 snAspThrThrglyGlnHisIleMetGluAspLeuAspThrAsnAlaasp 68
   ::::: ::::: ||||| :::::
214 AAGCAGCTGAGCTTGAGAGATTATCATGCTGATGGCGAGGCTAACCTG 263
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69 LysGlnLeuSerPheGlnGluPheIleMetLeuMetAlaArgLeuThrTr 85
   ||||| ::::: ||||| :::::
264 GGCCTCCACGAGGAAGATGACGAGGAGGTGACGAGGCGCTGCGCACACC 313
   ||||| ::::: ||||| :::::
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85 palSerHisGlnLysMetHisGlnGlyAspGlnGlyProGlyHisHisH 102
314 ATAAGCCAGGCTCGGGGAGCGCACCC 342
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102 IsLysProGlyLeuGlnGlnGlyThrPro 111
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seq_documentation_block:
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? GENERAL INFORMATION:
? APPLICANT: Hyseq, Inc
? TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
? FILE REFERENCE: 21272-066
? CURRENT APPLICATION NUMBER: PCT/US01/08656
? CURRENT FILING DATE: 2001-04-16
? PRIOR APPLICATION NUMBER: 09/522,929
? PRIOR FILING DATE: 2000-04-18
? PRIOR APPLICATION NUMBER: 09/770,160
? PRIOR FILING DATE: 2001-01-26
? NUMBER OF SEQ ID NOS: 10994
? SOFTWARE: Custom
? SEQ ID NO 6984
? LENGTH: 153
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: DOMAIN
? LOCATION: (38)..(75)
? OTHER INFORMATION: S-100/TCABP type calcium binding protein domain identified by
? OTHER INFORMATION: EMATRIX, accession number BL00303A, p-value=8.525e-12, raw sco
? OTHER INFORMATION: of 21.77
? NAME/KEY: DOMAIN
? LOCATION: (36)..(86)
? OTHER INFORMATION: S-100/TCABP type calcium binding protein domain identified by Pfam,
? OTHER INFORMATION: accession name S_100, E-value=0.0021, Pfam score of 21.6
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? OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08656-6984
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    Ratio: 3.286        Gaps: 7
Percent Similarity: 78.689    Percent Identity: 63.115
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alignment_block:
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Align seg 1/1 to: PCT-US01-08656-6984 from: 1 to: 153

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   ||||| |||||
48 eAsnThrSerHisGlnTyrSerValLysLeuGlnHisProAspThrLeuA 65
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148 AAGAAGAGAGAAATAAGATGAAGAAGTCATRGAACACATCATGAGGACCT 197
   ||||| |||||
82 LysLysGlnAsnLysAsnGlnLysValIleGlnHisIleMetArgGlyPr 98
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198 GGACACA...AATGCAGACAG.....CAGCTGAGCTTGAGGAGTTCA 238
   ||| ||||| :::::
98 ogLThrGlnAsnAlaIleGlnProAlaGlnLeuSer...ArgGluPheI 114
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239 TCATGCTGATGGCGAGGCTAACCTGGGCTTC.....CACGAGAAGATG 282
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/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-205-519-161	355.50	616.73	7.1e-26	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-205-519-161	355.50	616.75	7.1e-26	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-203-1337-139519	351.00	613.75	1.8e-25	
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/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-182-993-27568	429.00	404.98	1.1e-13	
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/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-182-993-35266	429.00	404.98	1.1e-13	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-182-993-35266	429.00	404.98	1.1e-13	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-182-993-25567	429.00	404.98	1.1e-13	
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/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-203-1337-36372	429.00	404.98	1.1e-13	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-203-1337-36372	429.00	404.98	1.1e-13	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-203-1339-34930	229.00	404.98	1.1e-13	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-203-1339-34930	229.00	404.98	1.1e-13	
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/cgn2_6/ptoddata/1/paa/US09_NEW_COMB.pep:US-09-791-537-124512	216.00	373.78	2.3e-12	
/cgn2_6/ptoddata/1/paa/US09_NEW_COMB.pep:US-09-791-537-124512	216.00	373.78	2.3e-12	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-077-600-2	214.50	373.40	3.1e-12	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-077-600-2	214.50	373.40	3.1e-12	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-030-937-19	214.50	373.40	3.1e-12	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-030-937-19	214.50	373.40	3.1e-12	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-030-937-23	214.50	373.40	3.1e-12	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10-030-937-23	214.50	373.40	3.1e-12	
/cgn2_6/ptoddata/1/paa/US09_NEW_COMB.pep:US-09-791-537-101828	213.50	371.75	3.9e-12	
/cgn2_6/ptoddata/1/paa/US09_NEW_COMB.pep:US-09-791-537-101828	213.50	371.75	3.9e-12	
/cgn2_6/ptoddata/1/paa/US09_NEW_COMB.pep:US-09-791-537-99618	211.50	368.18	6.1e-12	
/cgn2_6/ptoddata/1/paa/US09_NEW_COMB.pep:US-09-791-537-99618	211.50	368.18	6.1e-12	
/cgn2_6/ptoddata/1/paa/US10_NEW_COMB.pep:US-10				

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seq_name: /cogn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-139803

seq_documentation_block:
; Sequence 139803, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 139803
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-791-537-139803
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alignment_scores:
    Quality: 378.50      Length: 109
    Ratio: 4.027         Gaps: 1
    Percent Similarity: 86.239      Percent Identity: 69.725
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alignment_block:

US-09-806-382A-2 x US-09-791-537-139803 ..

Align seg 1/1 to: US-09-791-537-139803 from: 1 to: 122

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13 ATGTGCGACCTGGACGACACATAGACCATCATCAGACCTTCACGCA 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetSerGlnMetGlnSerSerIleGluThrIleIleAsnIlePheHisG1 17
63 ATACTCTGTGAAGCTGGGCGACCCAGACACCCGTGAACGAGGGGAATTCA 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 ntyrSerValArgLeuGlyHisTyrAspThrLeuIleGlnLysGlnSerL 34
113 AAGAGCTGTGCGAAGATCTGCAGAAATTTTCTCAAGAAGAGAAATTAAG 162
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 ysgLInleuValGlnLysGlnLeuProAsnPheLeuLysGlnLysLys 50
163 AATGAAAGTCAATAGACACATCATGAGAGACCTTGAGACAAATGACAGA 212
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 AasnGluAlaIleAsnGlnIleMetGlnAspLeuAspThrAsnValAs 67
213 CAGACGAGTGTGAGAGTTCATGCTGATGCGGAGGCTAACCT 262
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 ptySGlnLeuSerPheGlnGlnPheIleMetLeuValAlaArgLeuThrV 84
263 GGGCTCTCCACGAGAAATGACAGAG...GGTGACGAGGCGCTTGSCAC 309
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 aAlaSerHisGlnGlnMetHisAsnThrAlaProProGlnGlnLysHis 100
310 CACCATAGCCAGGCTCGGGAGAGGC 336
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 ArgHisGlnLysProGlnLysGlnLysGly 109
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seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pap:US-10-205-219-161

seq_documentation_block:

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; Sequence 161, Application US/10205219
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alstair
; APPLICANT: Brooksbank, Robert
; TITLE OF INVENTION: Identification and use of molecules implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 161
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Intracellular calcium binding protein
US-10-205-219-161
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alignment_scores:

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Quality: 355.50      Length: 107
Ratio: 3.864         Gaps: 1
Percent Similarity: 85.981      Percent Identity: 64.486
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alignment_block:

US-09-806-382A-2 x US-10-205-219-161 ..

Align seg 1/1 to: US-10-205-219-161 from: 1 to: 112

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16 TCGGAGCTGGACGACACATAGACCATCATCAGACCTTCACGCAATA 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
7 SerGlnLeuGlnArgSerIleSerThrIleIleAsnValPheHisGlnTy 23
66 CTCTGTGAAGCTGGGCGACCCAGACACCCGTGAACGAGGGGAATTCAAG 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
23 rSerArgLysTyrGlnHisProAspThrLeuAsnLysAlaGlnPheLysG 40
116 AGCTGTGCGAAGATCTGCAGAAATTTTCTCAAGAAGAGAAATTAAGAT 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
40 lMetValAsnLysAspLeuProAsnPheLeuLysArgGlnLysArgAsn 56
166 GAAAGGTCATAGACACATCATGAGAGCTTGACACAAATGACAGAA 215
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
57 GluAsnLeuLeuArgAspIleMetGlnAspLeuAspThrAsnGlnAspAs 73
216 GCAGCTGAGCTTGAGAGTTCATGCTGATGCGGAGGCTAACCTGGG 265
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
73 nGlnLeuSerPheGlnGlnLysMetLeuMetGlnLysLeuIlePheA 90
266 CCTCCGACGAGAAATGACAGAGGTGACAGGCGCTTGCCACACCAT 315
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
90 lacyHisGlnLysLysGlnLysGlnLysGly 112
316 AAGCCAGGCTCGGGAGAGGC 336
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
106 ArgHisGlnLysGlnLysGlnLysGly 112
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pap:US-09-791-537-139519

seq_documentation_block:

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; Sequence 139519, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomedix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139519
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-791-537-139519
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alignment_scores:
    Quality: 355.50      Length: 107
    Ratio: 3.864         Gaps: 1
    Percent Similarity: 85.981      Percent Identity: 64.486
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alignment_block:

US-09-806-382A-2 x US-09-791-537-139519 ..

Align seg 1/1 to: US-09-791-537-139519 from: 1 to: 113

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16 TCGGAGCTGGACGACACATAGACCATCATCAGACCTTCACGCAATA 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
7 SerGlnLeuGlnArgSerIleSerThrIleIleAsnValPheHisGlnTy 23
```

```
66 CTCTGTGAAGCTGGGCGACCGACACCTGAACCGAGGGGGAATTCAG 115
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
23 rSerAgtGlyTYrGlyHisProAspThrLeuAsnLysAlaGluPheLysG 40
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
116 AGCTGTGGCGAAAGATGTGCAAAATTTTCTCAGAGAGGAGTAAGAT 165
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
40 lMetValAsnLysAspLeuProAsnPheLeuLysArgGluLysArgAsn 56
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
166 GAAAGGTCATAGACACATCATGAGGACCTGGACACAAATGCGACACA 215
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
57 GluAsnLeuLeuArgAspIleMetGluAspLeuAspThrAsnGlnAspAs 73
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
216 GCAGCTGAGGTTGAGGAGTTCATGCTGATGGGAGGCTTAACCTGGG 265
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
73 ngIleuSerPheGluGluCysMetLeuMetGlyLysLeuIlePheA 90
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
266 CCTCCACGACGAGATGACAGAGGTGACGAGGCGCTGCGCACCCAT 315
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
90 lAcylHisGluLysLeuHisGluAsnAsnPro...ArgGlyHisAspHis 105
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
316 AGCCAGGCGCTCGGGAGGCGC 336
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
106 ArgHisGlyLysGlyCysGly 112
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-182-995-26821

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seq_documentation_block:
; Sequence 26821, Application US/10182995
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 1
; CURRENT APPLICATION NUMBER: US/10/182,995
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 29119
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26821
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011666.18
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P06702, EVALU 2.00e-34
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: A1720432.1, EVALU 2.00e-33
; US-10-182-995-26821
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alignment_scores:
Quality: 351.00 Length: 64
Ratio: 5.484 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-806-382a-2 x US-10-182-995-26821 ..

Align seg 1/1 to: US-10-182-995-26821 from: 1 to: 64

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151 AAGGAGATTAAGATGAAAGTGCATAGACACATCATGGAGGACCTCGGA 200
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 LysGluAsnLysAsnGluLysValIleGlnHisIleMetGluAspLeuAs 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 CACAAATGCACAGACAGCTGAGCTTCGAGAGTTCATGCTGATGG 250
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 PThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetA 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 lArgLeuThrTrpAlaSerHisGluLysMetHisGluGlyAspGluGly 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 CCTGCCACACACATTAAGCCAGGCGCTCGGGAGGCGCACCCCGC 342
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 ProGlyHisHisHisLysProGlyLeuGlyGluGlyThrPro 64
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-203-134-34897

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seq_documentation_block:
; Sequence 34897, Application US/10203134
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: PB 0004 WO 6
; CURRENT APPLICATION NUMBER: US/10/203,134
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38628
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 34897
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011666.18
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1e+02
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P06702, EVALU 2.00e-34
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: A1720432.1, EVALU 2.00e-33
; US-10-203-134-34897
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alignment_scores:
Quality: 351.00 Length: 64
Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-2 x US-10-203-134-34897

Align seg 1/1 to: US-10-203-134-34897 from: 1 to: 64

```
151 AAGGAGATAGATGAAGGTGATAGACACATCATGAGGAGCTGGA 200
|||||
1  LysGluSnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAAATGCAGACAGACAGCTGAGCTTCGAGAGTTGATCATGCTGATGG 250
|||||
17 pPrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetA 34
251 CGAGGCTAACCTGGGCTCCACAGAGAGATGCACGAGGGTGAAGAGGC 300
|||||
34 IaArgLeuThrTrpAlaSerHisGluLysMetHisGluGluAspGluGly 50
301 CCTGGCCACCACCATAGCCAGGCTCGGGAGGACCCCC 342
|||||
51 ProGlyHisHisLysProGlyLeuGlyGluGlyThrPro 64
```

seq_name: /cgn2.6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-203-136-35026

seq_documentation_block:

Sequence 35026, Application US/10203136

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: PB 0004 WO 3

CURRENT APPLICATION NUMBER: US/10/203,136

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38578

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 35026

LENGTH: 64

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: MAP TO AC011666.18

FEATURE: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

FEATURE: OTHER INFORMATION: SWISSPROT HIT: P06702, EVALUE 2.00e-34

FEATURE: OTHER INFORMATION: SWISSPROT HIT: P06702, EVALUE 2.00e-34

FEATURE: OTHER INFORMATION: SWISSPROT HIT: P06702, EVALUE 2.00e-34

FEATURE: OTHER INFORMATION: EST_HUMAN HIT: A1720432.1, EVALUE 2.00e-33

US-10-203-136-35026

alignment_scores:

Quality: 351.00 Length: 64
Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-2 x US-10-203-136-35026

Align seg 1/1 to: US-10-203-136-35026 from: 1 to: 64

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151 AAGGAGATAGATGAAGGTGATAGACACATCATGAGGAGCTGGA 200
|||||
1  LysGluSnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAAATGCAGACAGACAGCTGAGCTTCGAGAGTTGATCATGCTGATGG 250
|||||
17 pPrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetA 34
251 CGAGGCTAACCTGGGCTCCACAGAGAGATGCACGAGGGTGAAGAGGC 300
|||||
34 IaArgLeuThrTrpAlaSerHisGluLysMetHisGluGluAspGluGly 50
301 CCTGGCCACCACCATAGCCAGGCTCGGGAGGACCCCC 342
|||||
51 ProGlyHisHisLysProGlyLeuGlyGluGlyThrPro 64
```

seq_name: /cgn2.6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-182-993-33897

seq_documentation_block:

Sequence 33897, Application US/10182993

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

FILE REFERENCE: PB 0004 WO 2

CURRENT APPLICATION NUMBER: US/10/182,993

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 37811

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 33897

LENGTH: 64

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: MAP TO AC011666.18

FEATURE: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4

FEATURE: OTHER INFORMATION: SWISSPROT HIT: P06702, EVALUE 2.00e-34

FEATURE: OTHER INFORMATION: SWISSPROT HIT: P06702, EVALUE 2.00e-34

FEATURE: OTHER INFORMATION: SWISSPROT HIT: P06702, EVALUE 2.00e-34

FEATURE: OTHER INFORMATION: EST_HUMAN HIT: A1720432.1, EVALUE 2.00e-33

US-10-182-993-33897

alignment_scores:

Quality: 351.00 Length: 64
Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-2 x US-10-182-993-33897 ..

Align seg 1/1 to: US-10-182-993-33897 from: 1 to: 64

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151 AAGGAGATAGATGAAAGGTGATGACACATCATGAGGACCTGGA 200
|||||
1 LysGluAsnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAAATGACAGACAGCCTGAGGAGTTCATCATGCTGATGG 250
|||||
17 pThrAsnAlaAspLysGlnLeuSerPheGluIupPheIleMetLeuMetA 34
251 CGAGGCTAACCTGGGCTCCACAGAGAAATGACAGAGGTGACGAGGC 300
|||||
34 laArgLeuThrTrpAlaSerHisGlnLysMetHisGlnGlyAspGlnGly 50
301 CCGGCCACACCATTAAGCCAGGCTCGGGAGGCGACCCCC 342
|||||
51 ProGlyHisHisHisLysProGlyLeuGlyGlnGlyThrPro 64
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seq_name: /cgn2_6/plodata/1/paa/US10_NEW_COMB.pep:US-10-182-997-25178

seq_documentation_block:

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; Sequence 25178, Application US/10182997
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 10
; CURRENT APPLICATION NUMBER: US/10/182,997
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 26941
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 25178
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011666.18
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P06702, EVALU2 2.00e-34
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: A1720432.1, EVALU2 2.00e-33
; US-10-182-997-25178
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alignment_scores: Quality: 351.00 Length: 64
 Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block: US-09-806-382A-2 x US-10-182-997-25178 ..

Align seg 1/1 to: US-10-182-997-25178 from: 1 to: 64

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151 AAGGAGATAGATGAAAGGTGATGACACATCATGAGGACCTGGA 200
|||||
1 LysGluAsnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAAATGACAGACAGCCTGAGGAGTTCATCATGCTGATGG 250
|||||
17 pThrAsnAlaAspLysGlnLeuSerPheGluIupPheIleMetLeuMetA 34
251 CGAGGCTAACCTGGGCTCCACAGAGAAATGACAGAGGTGACGAGGC 300
|||||
34 laArgLeuThrTrpAlaSerHisGlnLysMetHisGlnGlyAspGlnGly 50
301 CCGGCCACACCATTAAGCCAGGCTCGGGAGGCGACCCCC 342
|||||
51 ProGlyHisHisHisLysProGlyLeuGlyGlnGlyThrPro 64
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seq_name: /cgn2_6/plodata/1/paa/US10_NEW_COMB.pep:US-10-203-135-34094

seq_documentation_block:

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; Sequence 34094, Application US/10203135
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: PB 0004 WO 5
; CURRENT APPLICATION NUMBER: US/10/203,135
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37012
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 34094
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011666.18
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.2
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P06702, EVALU2 2.00e-34
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: A1720432.1, EVALU2 2.00e-33
; US-10-203-135-34094
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alignment_scores: Quality: 351.00 Length: 64
 Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block: US-09-806-382A-2 x US-10-203-135-34094 ..

Align seg 1/1 to: US-10-203-135-34094 from: 1 to: 64

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151 AAGGAGATTAAGATGAAAAGTCAATAGAACATCATGTGAGGAGCCTGGA 200
|||||
1 LysGlnAsnLysAsnGlnLysValIleGlnHisIleMetGlnAspLeuAs 17
201 CACAAATGCAGACAGACAGCTGAGCTTCGAGAGATTCAATCATGTGATGG 250
|||||
17 pThrAsnAlaAspLysGlnLeuSerPheGlnLuphelleMetLeuMeTa 34
251 CGAGGCTAACCTGGGCTCCACGAGAGATGCACGAGGTCAGACAGGC 300
|||||
34 laArgLeuThrTrpAlaSerHisGlnLysMetHisGlnLysAspGlnGly 50
301 CCTGGCCACACCATTAAGCCAGGCTCGGGAGGACACCC 342
|||||
51 ProGlnHisHisLysProGlyLeuGlyGlnGlyThrPro 64

seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-203-137-34972
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seq_documentation_block:
; Sequence 34972, Application US/10203137
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: US/10/203,137
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 34972
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011666.18
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P06702, EVALU 2.00e-34
; OTHER INFORMATION: EST_HUMAN HIT: AI720432.1, EVALU 2.00e-33
; US-10-203-137-34972
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alignment_scores:
Quality: 351.00 Length: 64
Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-2 x US-10-203-137-34972 ..

Align seg 1/1 to: US-10-203-137-34972 from: 1 to: 64

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151 AAGGAGATTAAGATGAAAAGTCAATAGAACATCATGTGAGGAGCCTGGA 200
|||||
1 LysGlnAsnLysAsnGlnLysValIleGlnHisIleMetGlnAspLeuAs 17
201 CACAAATGCAGACAGACAGCTGAGCTTCGAGAGATTCAATCATGTGATGG 250
|||||
17 pThrAsnAlaAspLysGlnLeuSerPheGlnLuphelleMetLeuMeTa 34
251 CGAGGCTAACCTGGGCTCCACGAGAGATGCACGAGGTCAGACAGGC 300
|||||
34 laArgLeuThrTrpAlaSerHisGlnLysMetHisGlnLysAspGlnGly 50
301 CCTGGCCACACCATTAAGCCAGGCTCGGGAGGACACCC 342
|||||
51 ProGlnHisHisLysProGlyLeuGlyGlnGlyThrPro 64

seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-203-139-33565
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seq_documentation_block:
; Sequence 33565, Application US/10203139
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: PB 0004 WO 4
; CURRENT APPLICATION NUMBER: US/10/203,139
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37156
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 33565
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011666.18
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P06702, EVALU 2.00e-34
; OTHER INFORMATION: EST_HUMAN HIT: AI720432.1, EVALU 2.00e-33
; US-10-203-139-33565
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alignment_scores:
Quality: 351.00 Length: 64
Ratio: 5.484 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-2 x US-10-203-139-33565 ..

Align seg 1/1 to: US-10-203-139-33565 from: 1 to: 64


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151 AAGGAGATAGATGATAAGGTCATAGACATCATGAGAGACCTGGA 200
|||||
1 LysGluAsnLysAsnGluLysValIleGluHisIleMetGluAspLeuAs 17
201 CACAATGACAGACAGACAGCTGAGCTGAGAGAGTTCATCATGCTGATGG 250
|||||
17 pPhrsmAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMet 34
251 CGAGGCTAACTGGGCTCCCAAGAGATGCACAGAGGGTGACAGCGGC 300
|||||
34 laArgLeuThrTrpAlaSerHisGluLysMetHisGluGluLysPrluGly 50
301 CCTGGCCACCAACCATAGACAGGCTCGGGAGGGCACCACC 342
|||||
51 ProGlyHisHisHisLysProGlyLeuGlyGluGlyThrPro 64

seq_name: /cgn2_6/ptodata/1/paa/us09_NEW_COMB.pap:us-09-791-537-139518

seq_documentation_block:
; Sequence 139518, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139518
; LENGTH: 113
; TYPE: PR
; ORGANISM: Mus musculus
; US-09-791-537-139518

alignment_scores:
Quality: 329.50 Length: 107
Ratio: 3.702 Gaps: 1
Percent Similarity: 83.178 Percent Identity: 59.813

alignment_block:
US-09-806-382a-2 x US-09-791-537-139518 ..
Align seg 1/1 to: US-09-791-537-139518 from: 1 to: 113

16 TCGAGCTGGAGCGCAACATAGAGACCATCATCAACACCTTCCACCATTA 65
|||||
7 SerGlnMetGluArgSerIleThrThrIleIleAspThrPheHisGlnI 23
66 CTCTGTGAAGCTGGGGCAGCCAGACACCTGTAACAGAGGGGAATTCAAG 115
|||||
23 rSerArgLysGluGluLysIleProAspThrLeuSerLysGluPheArg 40
116 AGCTGTGCGAAGAAAGATCTGCAAAATTTTCTCAAGAGAGAAATAGAA 165
|||||
40 lMetValGluAlaGlnLeuAlaThrPheMetLysLysGluLysArgAsn 56
166 GAAAGGTGCATAGAACACATCATGAGAGACCTGACACAAATGCGAACA 215
|||||
57 GluAlaLeuIleAsnAspIleMetGluAspLeuAspThrAsnGlnAspAs 73
216 GCAGCTGAGCTTGCAGAGATTTCATCATGCTGATGCGAGGCTAACTGGG 265
|||||
73 nGlnLeuSerPheGluGluLysLysMetLeuMetAlaLysLeuIlePheA 90
266 CCTCCACAGAGAAAGATGCACAGAGGGTGAC...GAGGGCCCTGGCCACAC 312
|||||
90 lAcysHisGluLysLeuHisGluAsnAsnProArgGlyHisGlyHisSer 106
313 CATAGCCAGGCTCGGGGAG 333
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111 ||| ||| |||
107 HisGlyLysGlyCysGlyLys 113

seq_name: /cgn2_6/ptodata/1/paa/us10_NEW_COMB.pap:us-10-134-841-3

seq_documentation_block:
; Sequence 3, Application US/10134841
; GENERAL INFORMATION:
; APPLICANT: HALLE, JORN-PETER
; APPLICANT: GOSPELT, ANDREAS
; TITLE OF INVENTION: MRP8/MRP14 heterodimer, or its
; TITLE OF INVENTION: individual components in combination, for treating and/or
; TITLE OF INVENTION: preventing skin diseases, wounds and/or wound-healing
; TITLE OF INVENTION: heterodimers
; FILE REFERENCE: 50125/031002
; CURRENT APPLICATION NUMBER: US/10/134,841
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/322,925
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: DE 10121254.2
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 113
; TYPE: PR
; ORGANISM: Mus musculus
; US-10-134-841-3

alignment_scores:
Quality: 329.50 Length: 107
Ratio: 3.702 Gaps: 1
Percent Similarity: 83.178 Percent Identity: 59.813

alignment_block:
US-09-806-382a-2 x US-10-134-841-3 ..
Align seg 1/1 to: US-10-134-841-3 from: 1 to: 113

16 TCGAGCTGGAGCGCAACATAGAGACCATCATCAACACCTTCCACCATTA 65
|||||
7 SerGlnMetGluArgSerIleThrThrIleIleAspThrPheHisGlnI 23
66 CTCTGTGAAGCTGGGGCAGCCAGACACCTGTAACAGAGGGGAATTCAAG 115
|||||
23 rSerArgLysGluGluLysIleProAspThrLeuSerLysGluPheArg 40
116 AGCTGTGCGAAGAAAGATCTGCAAAATTTTCTCAAGAGAGAAATAGAA 165
|||||
40 lMetValGluAlaGlnLeuAlaThrPheMetLysLysGluLysArgAsn 56
166 GAAAGGTGCATAGAACACATCATGAGAGACCTGACACAAATGCGAACA 215
|||||
57 GluAlaLeuIleAsnAspIleMetGluAspLeuAspThrAsnGlnAspAs 73
216 GCAGCTGAGCTTGCAGAGATTTCATCATGCTGATGCGAGGCTAACTGGG 265
|||||
73 nGlnLeuSerPheGluGluLysLysMetLeuMetAlaLysLeuIlePheA 90
266 CCTCCACAGAGAAAGATGCACAGAGGGTGAC...GAGGGCCCTGGCCACAC 312
|||||
90 lAcysHisGluLysLeuHisGluAsnAsnProArgGlyHisGlyHisSer 106
313 CATAGCCAGGCTCGGGGAG 333

107 HisGlyLysGlyCysGlyLys 113

seq_name: /cgn2_6/ptodata/1/paa/us09_NEW_COMB.pap:us-09-791-537-13822
seq_documentation_block:
; Sequence 13822, Application US/09791537
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13822
LENGTH: 118
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-791-537-13822

alignment_scores:
Quality: 328.00 Length: 102
Ratio: 3.859 Gaps: 1
Percent Similarity: 83.333 Percent Identity: 63.725

alignment_block:

US-09-806-382a-2 x US-09-791-537-13822 ..

Align seg 1/1 to: US-09-791-537-13822 from: 1 to: 118

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43 ATCATCAACACCTTCACCAATACCTCTGAAAGCTGGGCGACCCAGACAC 92
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 IleileasnllephenslgintyrserValArgvalGlyProArgAspse 17

93 CTTGAACACGAGGGAATTCAGAGAGCTGGCGAAAGATGTCAAAATT 142
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
17 rleuserGlnLysGlnPheLysGlnLeuValGlnLysGlnLeuHisAsn 34

143 TTCTCAGAAGAGAAATAAGATGAAGTCAATAGACACATCATGAG 192
||| | | | | | | | | | | | | | | | | | | | | | | | | | |
34 heluLysLysGlnAlaArgAspGlnLysAlaIleAsnAspIleMetGlu 50

193 GACCTGGAGACAAATGCAGACAGCTGAGCTTGAGAGATTTCATCAT 242
||| | | | | | | | | | | | | | | | | | | | | | | | | | |
51 AspLeuAspThrAsnGlnAspLysGlnLeuSerPheGlnGluPheValI 67

243 GCTGATGGCGAGGTTAACTGGGCTCCACGAGAGATGCAGAGGT 291
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
67 eleuMetAlaArgLeuValHisAlaSerHisGlnGlnMetHisLysAsn 84

292 .....GACGAGGCGCTGGCGACACCATAGCCAGGCTCGGGGAGG 336
: : : : : | | | | | | | | | | | | | | | | | | | | | |
84 laproHisAspHisGlnGlnHisSerHisGlyProGlnLysGlnGlySer 100

337 ACCCC 342
|||
101 GlyPro 102
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TELEFAX: (415) 854-0875

SEQUENCE CHARACTERISTICS:
 LENGTH: 64 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-200-016-6

alignment_scores:
 Quality: 351.00 Length: 64
 Ratio: 5.484 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-2 x US-08-200-016-6

Align seg 1/1 to: US-08-200-016-6 from: 1 to: 64

151 AAGGAAATAGAAATGAAAAAGTCATAGAACACATCATGAGACCTGGA 200
 ||||||||||||||||||||||||||||||||||||||||||||||||
 1 LysGluAsnLysAsnGluValIleGluHisIleMetGluAspLeuAs 17
 201 CACAATGACAGACAGCTGAGCTTCGAGAGATGACATCATGCTGATGG 250
 ||||||||||||||||||||||||||||||||||||||||||||||||
 17 pTrpAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMe 34
 251 CGAGGCTAACCTGGGCTCCACAGAGAGATGACAGAGGTGACGAGGCG 300
 ||||||||||||||||||||||||||||||||||||||||||||||||
 34 IaArgLeuThrTrpAlaSerHisGluLysMetHisGluLysAspGluGly 50
 301 CCGGCCACCCACCATTAAGCCAGGCTCGGGAGGCGACCCCC 342
 ||||||||||||||||||||||||||||||||||||||||||||||||
 51 ProGlyHisHisHisLysProGlyLeuGlyGluGlyThrPro 64

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-200-016-5

seq_documentation_block:

Sequence 5, Application US/08200016
 Patent No. 5614397
 GENERAL INFORMATION:
 APPLICANT: Weissman, Irving
 APPLICANT: Lagasse, Eric
 TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR MODULATING
 TITLE OF INVENTION: APOPTOSIS IN HEMATOLOGY CELLS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Fish & Richardson
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park
 STATE: California
 COUNTRY: US
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/200,016
 FILING DATE: 22-FEB-1994
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Rae-Ventler, Barbara
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: 06037/003001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 854-5277
 TELEFAX: (415) 854-0875
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-08-200-016-5

alignment_scores:
 Quality: 262.00 Length: 50
 Ratio: 5.240 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-2 x US-08-200-016-5

Align seg 1/1 to: US-08-200-016-5 from: 1 to: 50

1 ATGACTTGCAAAATGTGCGACGTGGAGCAACATAGACCATCATCA 50
 ||||||||||||||||||||||||||||||||||||||||||||||||
 1 MetThrCysLysMetSerGlnLeuGlnArgAsnIleGluThrIleIleAs 17
 17 nThrPheHisGlnTrpSerValLysLeuGlyHisProAspThrLeuAsnG 34
 51 CACCTTCACCAATATCTGTGAAGCTGGGGCACCACGACACCTGAAC 100
 ||||||||||||||||||||||||||||||||||||||||||||||||
 17 nThrPheHisGlnTrpSerValLysLeuGlyHisProAspThrLeuAsnG 34
 101 AGGGGATTTGCAAGAGCTGGCGAAAGATCTGCATAATTTCTCAAG 150
 ||||||||||||||||||||||||||||||||||||||||||||||||
 34 InglyGluPheLysGlnLeuValArgLysAspLeuGlnAsnPheLeuLys 50

seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-568-310D-20

seq_documentation_block:

Sequence 20, Application US/08568310D
 Patent No. 5976832
 GENERAL INFORMATION:
 APPLICANT: HITOMI, JIRO
 APPLICANT: YAMAGUCHI, KEN
 APPLICANT: YAMAMURA, TOKUJIRO
 APPLICANT: KIMURA, TATSUJI
 TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
 STREET: 99 PARK AVENUE
 CITY: NEW YORK CITY
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
 MEDIUM TYPE: STORAGE
 COMPUTER: IBM-PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS 6.2
 SOFTWARE: WORDPERFECT 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/568,310D
 FILING DATE: DECEMBER 6, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
 FILING DATE: 3/6/95 and 3/6/95, respectively
 ATTORNEY/AGENT INFORMATION:
 NAME: KLEIN, MILTON
 REGISTRATION NUMBER: 27101
 REFERENCE/DOCKET NUMBER: 3316
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)953-3350
 TELEFAX: (212)953-3352
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 92
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 20:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-20

alignment_scores:
Quality: 214.50 Length: 92
Ratio: 2.979 Gaps: 1
Percent Similarity: 78.261 Percent Identity: 46.739

alignment_block:
US-09-806-382A-2 x US-08-568-310D-20 ..

Align seg 1/1 to: US-08-568-310D-20 from: 1 to: 92

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13 ATGTCCAGCTGGAACGCAATAGACCATCATCAACACCTTCCACCA 62
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1 MetThrLysLeuGluGlnHisLeuGluGlyLeuAlaSnIlePheHsGl 17
63 ATACTGTGAAGCTGGGCGACCCAGACACCCGTGAACAGGAGGAATTCA 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 nTyrSerValArgLysGlyHisPheAspThrLeuSerLysGlyGluLeu 34
113 AAGAGCTGTGCGAAAGATCTGCAAAATTTCTCAAGAAGAGAAATAG 162
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 ysgInleuLeuThrLysGluLeuAlaSnThrIle...LysAsnIleLys 49
163 AATGAAAGGTGATAGACATCATGAGAGCCGTGACACAAATGCAGA 212
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
50 AspLysAlaValIleAspGluIlePheGlnGlyLeuAspAlaSnGlnAs 66
213 CAAGAGCTGAGCTTCGAGAGATTTCATGCTGATGCGAGGCTAACT 262
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
66 pgiuGlnValAspPheGlnGluPheIleSerLeuValAlaIleAlaLeu 83
263 GGGCCCTCCACGAGAAAGATGCACGAG 288
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83 ysaIlaIaIaHisTyrHisThrHisLys 91
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seq_name: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:US-09-270-455-20

seq_documentation_block:

Sequence 20, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 20: FROM 1 TO 92
US-09-270-455-20

alignment_scores:
Quality: 214.50 Length: 92
Ratio: 2.979 Gaps: 1
Percent Similarity: 78.261 Percent Identity: 46.739

alignment_block:
US-09-806-382A-2 x US-09-270-455-20 ..

Align seg 1/1 to: US-09-270-455-20 from: 1 to: 92

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1 MetThrLysLeuGluGlnHisLeuGluGlyLeuAlaSnIlePheHsGl 17
63 ATACTGTGAAGCTGGGCGACCCAGACACCCGTGAACAGGAGGAATTCA 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 nTyrSerValArgLysGlyHisPheAspThrLeuSerLysGlyGluLeu 34
113 AAGAGCTGTGCGAAAGATCTGCAAAATTTCTCAAGAAGAGAAATAG 162
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34 ysgInleuLeuThrLysGluLeuAlaSnThrIle...LysAsnIleLys 49
163 AATGAAAGGTGATAGACATCATGAGAGCCGTGACACAAATGCAGA 212
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
50 AspLysAlaValIleAspGluIlePheGlnGlyLeuAspAlaSnGlnAs 66
213 CAAGAGCTGAGCTTCGAGAGATTTCATGCTGATGCGAGGCTAACT 262
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
66 pgiuGlnValAspPheGlnGluPheIleSerLeuValAlaIleAlaLeu 83
263 GGGCCCTCCACGAGAAAGATGCACGAG 288
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
83 ysaIlaIaIaHisTyrHisThrHisLys 91
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seq_name: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:US-08-794-000-2

seq_documentation_block:

Sequence 2, Application US/08794000
Patent No. 6087123
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Metal-Containing Ribonucleotide Polypeptides
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,000
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE96/01337
FILING DATE: 17-JUL-1996

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 25 992.0
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 30 500.0
; FILING DATE: 18-AUG-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-794-000-2

alignment_scores:
  Quality: 213.50      Length: 91
  Ratio: 2.847        Gaps: 1
  Percent Similarity: 82.418  Percent Identity: 45.055

alignment_block:
US-09-806-382a-2 x US-08-794-000-2  ..

Align seg 1/1 to: US-08-794-000-2 from: 1 to: 91

16 TCGAGAGCTGAGCGCAACATAGACACATCATACACCTTCACCAATA 65
   ::::::::::::::::::::| | | | | | | | | | | | | | | |
1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGln 17
66 CTCTGTGAAGCTGGGGCACCAGACACCTGAAACAGGGGGAATTCAAG 115
   ||| | | | | | | | | | | | | | | | | | | | | | | |
17 rSerValArgLeuGlyHisTyrAspThrLeuIleLysArgGlnLeuLys 34
116 AGCTGGTGGCAAAAAGATTCGCAAAATTTCTCAAGAGAGGAATAAGAT 165
   ::| | | | | | | | | | | | | | | | | | | | | | | |
34 InLeuIleThrLysGlnLeuProAsnThrLeu...LysAsnThrLysAsp 49
166 GAAAGAGCTCATAGACACATCATGAGAGACCTGAGACAAATGCAGCAA 215
   ::| | | | | | | | | | | | | | | | | | | | | | | |
50 GlnGlyThrIleAspLysIlePheGlnAsnLeuAspLysGlnAspGln 66
216 GCAGCTGAGCTGCGAGAGTTTCATCATGCTGATGGCGAGGCTTAACCTG 265
   ::| | | | | | | | | | | | | | | | | | | | | | | |
66 uGlnValSerPheLysGlnPheValValLeuValThrAspValLeuL 83
266 CCTCCGACGAGAGATGACGAG 288
83 hAlaHisAspAsnIleHisLys 90

seq_name: /cgn2_6/plodata/2/1aa/5B_COMB.pep:US-08-568-310D-19

seq_documentation_block:
; Sequence 19, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
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; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564(both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 19:
; FROM 1 TO 92
; US-08-568-310D-19

alignment_scores:
  Quality: 211.50      Length: 92
  Ratio: 2.858        Gaps: 1
  Percent Similarity: 80.435  Percent Identity: 44.565

alignment_block:
US-09-806-382a-2 x US-08-568-310D-19  ..

Align seg 1/1 to: US-08-568-310D-19 from: 1 to: 92

13 ANGTCGACGCTGGAAGCGCAACATAGACCATCATCAACACCTTCACCA 62
   ||| | | | | | | | | | | | | | | | | | | | | |
1 MetThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGln 17
63 ATACTGTGGAAGCTGGGGCACCAGACACCTGAAACAGGGGGAATTCA 112
   ||| | | | | | | | | | | | | | | | | | | | | |
17 nTyrSerValArgValGlyHisPheAspThrLeuAsnLysArgGlnLeu 34
113 AAGAGCTGTGGCAAAAGATTCGCAAAATTTCTCAAGAGAGGAATAAG 162
   ||| | | | | | | | | | | | | | | | | | | | | |
34 yGlnLeuIleThrLysGlnLeuProLysThrLeu...GlnAsnThrLys 49
163 AATGAAAAGCTCATAGACACATCATGAGAGACCTGAGACAAATGCAGA 212
   ::| | | | | | | | | | | | | | | | | | | | | | | |
50 AspGlnProThrIleAspLysIlePheGlnAspLeuAspLysAspLys 66
213 CAAGCAGCTGAGCTTGCAGAGATTCATCATGCTGATGGCGAGGCTAACC 262
   | | | | | | | | | | | | | | | | | | | | | | | |
66 pGlyAlaValSerPheGlnGluPheValValLeuValSerArgValLeu 83
263 GGGCTCCGACGAGAGATGACGAG 288
83 yThrAlaHisIleAspIleHisLys 91

seq_name: /cgn2_6/plodata/2/1aa/6B_COMB.pep:US-09-270-455-19

seq_documentation_block:
; Sequence 19, Application US/09270455
; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
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APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92
US-09-270-455-19

alignment_scores:
Quality: 211.50 Length: 92
Ratio: 2.858 Gaps: 1
Percent Similarity: 80.435 Percent Identity: 44.565

alignment_block:

US-09-806-382A-2 x US-09-270-455-19 ..

Align seg 1/1 to: US-09-270-455-19 from: 1 to: 92

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1 MetThrLysLeuGluAspHisLeuGluGlyIleIleLsnIlePheHsIgl 17
63 ATATCTGTGAAGCTGGGCGACCCAGACACCTGAAACAGGGGGAATTCA 112
|||||
17 nTyrSerValArgValGlyIleHisPheAspThrIleuAsnLysArgGluLeu 34
113 AAGAGCTGGTGCAGAAAGATCTGCAAAATTTCTCAAGAAGAGAGATTAC 162
|||||
34 ysgInleuIleThrLysGluLeuProLysThrLeu...GlnAsnThrLys 49
163 AATGAAAGGCTATAGACACATCATGAGAGACCTGGACACAATTCACGA 212
|||||
50 AspGlnProThrIleAspLysIlePheGlnAspLeuAspAlaAspLysAs 66
213 CAAGCAGCTAGAGCTTGAGAGATTCAATGCTGATGGCGAGGCTAACCT 262
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66 pGlyAlaValSerPheGluIlePheValValLeuValSerArgValLeu 83
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263 GGGCTCCGACGAGAGATGACGAG 288
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83 ysrnAlaHisIleAspIleHisLys 91

seq_name: /cgn2_6/plodata/2/1aa/5B_COMB.pep:US-08-918-727-5

seq_documentation_block:

Sequence 5, Application US/08918727
Patent No. 5849528
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN S100 PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,727
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0373 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 337730
US-08-918-727-5

alignment_scores:
Quality: 177.50 Length: 88
Ratio: 2.536 Gaps: 1
Percent Similarity: 79.545 Percent Identity: 39.773

alignment_block:

US-09-806-382A-2 x US-08-918-727-5 ..

Align seg 1/1 to: US-08-918-727-5 from: 1 to: 92

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|||||
1 MetSerGluLeuGluLysAlaMetValAlaLeuIleAspValPheHsIgl 17
63 ATATCTGTGAAGCTGGGCGACCCAGACACCTGAAACAGGGGGAATTCA 112
|||||
17 nTyrSerGlyArgGluGlyAspLysHisLysLeuLysSerGluLeu 34
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113 AAGAGCTGTCGGAAGATCTGCAAAATTTTCTCAAGAGAGAAATAG 162
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 ysgluleuileasnsngluleuserhispheleu...gluglulelys 49
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
163 AATGAAAAGTCATAGACATCATGAGACCTGGAGCAGACACAAATGCGA 212
gluglingleuvalvalasplysvalmetglutrlleuaspsnasp1ylas 66
213 CAAGAGCTGAGCTTCGAGAGCTTCATCATGCTGATGAGCAGCTAACCT 262
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
66 pgl1yglucysasphneglulupheme1alapheta1alame1valthrt 83
263 GGGCCTCCACGAG 276
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83 hralacyshtsglu 87

seq_name: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:US-09-205-680A-5
seq_documentation_block:
; Sequence 5, Application US/09205680A
; Patent No. 6103497
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN S100 PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205.680A
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Colette C. Muenzen
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0373 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 337730
; US-09-205-680A-5

alignment_scores:
Quality: 177.50 Length: 88
Ratio: 2.536 Gaps: 1
Percent Similarity: 79.545 Percent Identity: 39.773

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alignment_block:
US-09-806-382A-2 x US-09-205-680A-5 ..
Align seg 1/1 to: US-09-205-680A-5 from: 1 to: 92

13 ATGTGCGAGCTGGAAGCAGACATAGAGCCATCATGCAACCTTCACCA 62
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1 Metsergluleuglulysalame1val1alaleu1leaspyal1pnehtsgl 17
63 ATACTCTGTGAAGCTGGGGCACCAGACACCCTGAGACAGGGGAATTCA 112
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
17 ntYserclYar9gluclYasplysh1slyslleu1ylsYsercluleu1 34
113 AAGAGCTGTCGGAAGATCTGCAAAATTTTCTCAAGAGAGAAATAG 162
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 ysgluleuileasnsngluleuserhispheleu...gluglulelys 49
163 AATGAAAAGTCATAGACATCATGAGAGCTTCGAGCAGACAAATGCGA 212
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50 gluglingleuvalvalasplysvalmetglutrlleuaspsnasp1ylas 66
213 CAAGAGCTGAGCTTCGAGAGCTTCATCATGCTGATGAGCAGCTAACCT 262
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
66 pgl1yglucysasphneglulupheme1alapheta1alame1valthrt 83
263 GGGCCTCCACGAG 276
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83 hralacyshtsglu 87

seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-09-051-589-1
seq_documentation_block:
; Sequence 1, Application US/09051589
; Patent No. 5990080
; GENERAL INFORMATION:
; APPLICANT: HAGLID, Kenneth G.
; TITLE OF INVENTION: USE OF PROTEIN S-100B IN MEDICINES CONTAINING THE
; FILE REFERENCE: 003300-478
; CURRENT APPLICATION NUMBER: US/09/051,589
; CURRENT FILING DATE: 1998-04-15
; EARLIER APPLICATION NUMBER: SE 9503620-8
; EARLIER FILING DATE: 1995-10-17
; EARLIER APPLICATION NUMBER: PCT/SE96/01305
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Protein S-100b
; US-09-051-589-1

alignment_scores:
Quality: 173.50 Length: 88
Ratio: 2.514 Gaps: 1
Percent Similarity: 78.409 Percent Identity: 38.636

alignment_block:
US-09-806-382A-2 x US-09-051-589-1 ..
Align seg 1/1 to: US-09-051-589-1 from: 1 to: 92

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 Metsergluleuglulysalame1val1alaleu1leaspyal1pnehtsgl 17
63 ATACTCTGTGAAGCTGGGGCACCAGACACCCTGAGACAGGGGAATTCA 112
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
17 ntYserclYar9gluclYasplysh1slyslleu1ylsYsercluleu1 34

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113 AACAGCTGGTGCAGAAAGATCTGCAAAATTTCTCAAGAGAGAAATAG 162
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34 yseluleuileasnsngluLeuSerHispheLeu...Glululilelys 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
163 AATGAAAGGTCTATAGACATCATGAGGAGGACCTGACCAATATGCAGA 212
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
50 GluGlulvalValaspluysValMetGluThrLeuAspGluAspGlyAs 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
213 CAAGCAGCTGCTCGAGGAGTTTCATCATGATGCGAGGCTAACCT 262
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
66 pgluylucysAspPheGlnGluPheMetAlaPheValSerMetValThr 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
263 GGGCTCCACGAG 276
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83 hralaCysHISglu 87

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seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-07-987-272A-11

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seq_documentation_block:
; Sequence 11, Application US/07987272A
; Patent No. 5731166
; GENERAL INFORMATION:
; APPLICANT: Ceczy, C., Simpson, R. J. and Lackmann, M
; TITLE OF INVENTION: No. 5731166el Chemolactic Factor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman Darby & Cushman
; STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,272A
; FILING DATE: 05-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 2127
; FILING DATE: 05-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 4463
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Blinkman, David W
; REGISTRATION NUMBER: 20,817
; REFERENCE/DOCKET NUMBER: DWB/1925/200259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861 3000
; TELEFAX: 202-822 0944
; TELETYPE: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-987-272A-11

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alignment_scores:

Quality:	172.50	Length:	87
Ratio:	2.500	Gaps:	1
Percent Similarity:	79.310	Percent Identity:	39.080

alignment_block:
US-09-806-382A-2 x US-07-987-272A-11

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1 SerGluLeuGluLysAlaMetValAlaLeuIleAspAlaPheHisGlnTy 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
66 CTCTGTGAACCTGGGCGCCACAGACACCTGAACCGAGGGGAATTCAAG 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 rserGlyArgGluGlyAspLysHisLysLeuLysLysSerGluLeuysG 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
116 AGCTGTGCGCAAAAGATCTGCAAAATTTCTCAAGAAGAGCAATAGCAAT 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 lueuileasnsngluLeuSerHispheLeu...GlululilelysGlu 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
166 GAAAGGTCTATAGACATCATGAGGAGGACCTGACCAATATGCAGCAA 215
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
50 GluGluValValaspluysValMetGluThrLeuAspAsnAspGlyAspG 66
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216 GCAGCTGAGCTCGAGGAGTTTCATCATGATGCGAGGCTAACCTGGG 265
||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
66 yluLysAspPheGlnGluPheMetAlaPheValAlaMetValThrThra 83
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266 CCTCCACGAG 276
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83 lacYshISglu 86

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seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-07-662-198B-2

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seq_documentation_block:
; Sequence 2, Application US/07662198B
; Patent No. 5262528
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; APPLICANT: Lee, Sam W.
; APPLICANT: Tomasetto, Catherine
; TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb
; OPERATING SYSTEM: IBM PS/2 Model 502 or 55SX
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/662,198B
; FILING DATE: 19910228
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/049001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELETYPE: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
US-07-662-198B-2

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alignment_scores:

Quality: 154.50 Length: 82
Ratio: 2.414 Gaps: 1
Percent Similarity: 78.049 Percent Identity: 36.585

alignment_block:

US-09-806-382A-2 x US-07-662-198B-2 ..

Align seg 1/1 to: US-07-662-198B-2 from: 1 to: 97

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3 SerSerLeuclnclnAlaLeuAlaValThrThrPheHisLysIy 19
||| : : : ||| |||: : : : : : : : : : : : : : : :
66 CTCTGTGAAGCTGGGGCCACCCAGACACCTGAACGAGGGGAATTCAAG 115
||| : : : ||| |||: : : : : : : : : : : : : : : :
19 rSerCysGlnGlnGlyAspLysPheLysLeuSerLysGlyGluMetLys 36
|||||: : : : : : : : : : : : : : : : : : : : :
116 AGCTGGTGGCAAAAGATCTGCAGAAATTTCTCAAGAGAGAGATAGAA 165
|||||: : : : : : : : : : : : : : : : : : : : :
36 IuLeuLeuHisLysGluLeuProSerPheVal...GlyGluLysValAsp 51
|||||: : : : : : : : : : : : : : : : : : : : :
166 GAAAGGTCATAGACACATCATGAGAGAGAGAGAGAGAGAGAGAGACA 215
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52 GlnGlnGlyLeuLysLysLeuMetGlyAsnLeuAspGlnAsnSerAsp 68
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216 GCAGCTGAGGCTTCGAGAGGTCATCATGCTGATGAGGAGGCTAACC 261
|||||: : : : : : : : : : : : : : : : : : : : :
68 nGlnValAspPheGlnGlnIuTyrrAlaValPheLeuAlaLeuIleThr 83
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seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-190-560-2

seq_documentation_block:

; Sequence 2, Application US/08190560

; Patent No. 5798257

; GENERAL INFORMATION:

; APPLICANT: Zain, Sayeeda

; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: United States

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/190,560

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Digilio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 78792Y

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 101 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-190-560-2

alignment_scores:

Quality: 150.50 Length: 103
Ratio: 2.007 Gaps: 4
Percent Similarity: 72.816 Percent Identity: 33.010

alignment_block:

US-09-806-382A-2 x US-08-190-560-2 ..

Align seg 1/1 to: US-08-190-560-2 from: 1 to: 101

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1 MetAlaCys.....ProLeuGluLysAlaLeuAspValMetValSe 14
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51 CACCTTCACCAATATCTGTGAAGCTGGGGCCACCCAGACACCTGAACC 100
|||||: : : : : : : : : : : : : : : : : : : : :
14 rThrPheHisLysIyTrSerGlyLysGlnGlyAspLysPheLysLeuAsn 31
|||||: : : : : : : : : : : : : : : : : : : : :
101 AGGGGAATTCAAGAGAGCTGTGCGCAAAAGATCTGCAGAAATTTTCTCA 150
|||||: : : : : : : : : : : : : : : : : : : : :
31 ySerGluLeuLysGluLeuLeuThrArgGluLeuProSerPheLeuGly 47
|||||: : : : : : : : : : : : : : : : : : : : :
151 AAGGAGATTAAGATGAAAAGTCTATAGACATCATGAGAGAGCTGGA 200
|||||: : : : : : : : : : : : : : : : : : : : :
48 LysArgThr...AspGluAlaAlaPheGlnLysLeuMetSerAsnLeuAs 63
|||||: : : : : : : : : : : : : : : : : : : : :
201 CACAATATGACAGACAGAGCTGAGCTTCGAGAGAGTTCATCATGCTGAT 250
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63 pSerAsnArgAspAsnGlnValAspPheGlnGlnIuTyrcysValPheLeu 80
|||||: : : : : : : : : : : : : : : : : : : : :
251 CGAGGCTAACCTGGGCTCCACGAGAGAGATGCAGAGGTT.....GAC 294
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80 erCysIleAlaMetMetCysAsnGln...PhepGlnGlyPheProAsp 95
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295 GAGGGCCCT 303
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96 LysGlnPro 98
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100

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 06:44:07 ; Search time 66.65 Seconds
(without alignments)
1271.471 Million cell updates/sec

Title: US-09-806-382A-2

Perfect score: 345
Sequence: 1 atgacttgcaaatgtcgca.....tcggaggagcaccctca 345

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents.NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345	100.0	571	1	US-08-385-241-4 Sequence 4, Appl1
2	197	57.1	4440	1	US-08-200-016-4 Sequence 4, Appl1
3	98.8	28.6	273	3	US-08-794-000-3 Sequence 3, Appl1
4	93.2	27.0	429	2	US-08-568-310D-1 Sequence 1, Appl1
5	93.2	27.0	429	4	US-09-270-455-1 Sequence 1, Appl1
6	77.4	22.4	441	2	US-08-568-310D-12 Sequence 12, Appl1
7	77.4	22.4	441	4	US-09-270-455-12 Sequence 12, Appl1
8	56.2	16.3	452	1	US-07-662-198B-1 Sequence 1, Appl1
9	56.2	16.3	452	1	US-08-332-742-1 Sequence 1, Appl1
10	47	13.6	579	1	US-08-190-560-3 Sequence 3, Appl1
11	47	13.6	579	1	US-08-469-277-3 Sequence 3, Appl1
12	47	13.6	579	2	US-08-468-946-3 Sequence 3, Appl1
13	47	13.6	579	2	US-08-468-942-3 Sequence 3, Appl1
14	46.6	13.5	10952	1	US-08-602-036A-1 Sequence 1, Appl1
15	46.6	13.5	10952	2	US-08-502-374A-1 Sequence 1, Appl1
16	46.6	13.5	10952	2	US-08-642-407A-1 Sequence 1, Appl1
17	46.4	13.4	1141	2	US-08-918-727-4 Sequence 4, Appl1
18	46.4	13.4	1141	3	US-09-205-680A-4 Sequence 4, Appl1
19	45	13.0	303	1	US-08-190-560-1 Sequence 1, Appl1
20	45	13.0	303	2	US-08-469-277-1 Sequence 1, Appl1
21	45	13.0	303	1	US-08-468-946-1 Sequence 1, Appl1
22	45	13.0	303	2	US-08-468-942-1 Sequence 1, Appl1
23	43.4	12.6	5552	3	US-08-155-888-1 Sequence 1, Appl1
24	43	12.5	347	4	US-09-328-111-848 Sequence 848, App
25	41.2	11.9	7218	1	US-08-232-463-14 Sequence 14, Appl1
26	41	11.9	408	1	US-08-385-241-2 Sequence 2, Appl1
27	41	11.9	418	1	US-07-987-272A-15 Sequence 15, Appl1

28	40	11.6	3176	1	US-08-425-299A-3 Sequence 3, Appl1
29	40	11.6	3176	2	US-08-486-663A-14 Sequence 14, Appl1
30	40	11.6	3176	2	US-08-247-904B-13 Sequence 13, Appl1
31	40	11.6	3176	3	US-08-767-942A-14 Sequence 14, Appl1
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33	39.8	11.5	1080	3	US-09-205-680A-2 Sequence 2, Appl1
34	39.6	11.5	433	1	US-07-987-272A-13 Sequence 13, Appl1
35	38.4	11.1	3176	2	US-09-070-060-10 Sequence 10, Appl1
36	38.4	11.1	3177	3	US-09-357-746-10 Sequence 10, Appl1
37	37.8	11.0	289	4	US-09-007-005-17 Sequence 17, Appl1
38	37.8	11.0	289	4	US-09-244-796-17 Sequence 17, Appl1
39	35	10.1	4195	1	US-08-200-016-1 Sequence 1, Appl1
40	34.2	9.9	1302	1	US-08-913-050A-2 Sequence 2, Appl1
41	34.2	9.9	1466	2	US-08-749-902-2 Sequence 2, Appl1
42	33.8	9.8	1114	3	US-09-048-889-10 Sequence 10, Appl1
43	33.6	9.7	2589	2	US-08-482-728A-3 Sequence 3, Appl1
44	33	9.6	1599	3	US-08-853-733B-1 Sequence 1, Appl1
45	33	9.6	1603	1	US-08-625-209A-1 Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-385-241-4
Sequence 4, Application US/08385241
Patent No. 5776348
GENERAL INFORMATION:
APPLICANT: Selengut Ph.D., Jeremy D.
APPLICANT: Orme-Johnson Ph.D., William H.
APPLICANT: Dretler M.D., Stephen P.
APPLICANT: Asakura M.D., Hirokaka
TITLE OF INVENTION: SYSTEM AND METHOD FOR INHIBITING
FORMATION OF CRYSTALLINE STRUCTURES THAT INCLUDE STRUTITE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate Hall & Stewart
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,241
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Herschbach Ph.D., Brenda M.
REGISTRATION NUMBER: P-39,223
REFERENCE/DOCKET NUMBER: 492611-000 (MIT6915)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5175
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 571 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hMRP-14 CDNA
US-08-385-241-4
Query Match 100.0%, Score 345, DB 1, Length 571;

Best Local Similarity 100.0%; Pred. No. 7.6e-92;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 44 ATGATTGCAAAATGCTCCAGCTGGACGCAACATAGAGACCATCATCAACACCTTCCAC 103
QY 61 caatcctctgaaagctggggaacccagacacccctgaaccaggggaattcctaaagagctg 120
Db 104 CAATCTCTGTGAAGCTGGGGCACCAGACACCTTGAACCAAGGGGAATTCAAAGAGCTG 163
QY 121 gtgcgaaagatctgcgaaatttctcaagaaggaataaagatgaaaggtcagaa 180
Db 164 GTGCAAAAGATCTGCAAAATTTTCTCAAGAAAGAGAAATGAAGTAAAGGTATAGAA 223
QY 181 caccatcagagagagctgagacacaaatgcaagaacagcagctgagattctgagagctc 240
Db 224 CACATCATGAGAGAGAGCTGACACAAATGACAGCAAGCAGCTGAGCTTGAGAGACTTCATC 283
QY 241 atgctgatgagagagctgaacctgagccctccacagagaagatgcagagaggtgacagagc 300
Db 284 ATGCTGATGGGAGGAGCTTAACCTGGGCTCTCCACAGAAAGATGCAGAGGCTGACAGAGGC 343
QY 301 cctggcacaaccataagccagcctcgaggagggcacccctaa 345
Db 344 CTGGCCACACACATAAAGCCAGGCTCGGGAGGACACCCCTAA 388
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RESULT 2
US-08-200-016-4
Sequence 4, Application US/08200016
Patent No. 5614397

GENERAL INFORMATION:
APPLICANT: Weissman, Irving
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: APOPTOSIS IN HEMATOLOGY CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200.016
FILING DATE: 22-FEB-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 06037/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2738
OTHER INFORMATION: /note= "Nucleotide indicated as "N"
OTHER INFORMATION: represents a region of 360 base pairs which do not

OTHER INFORMATION: appear in Figure 2."
US-08-200-016-4

Query Match 57.1%; Score 197; DB 1; Length 4440;
Best Local Similarity 100.0%; Pred. No. 3.8e-48;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 149 aagaagagaataagaatgaagaagtcataagaacacatcatgtgagagcctggacacaatg 208
Db 3447 AGAAGGAGATTAAGATGAAGAGTATGAACACATCATGTGAGAGACCTGGACACAAATG 3506
QY 209 cagacaagcagctgagcttcgagagagttcatcatgtgagtcgagagctgaacctggcct 268
Db 3507 CAGACAGAGAGCTGAGCTTCGAGAGATTTCATCATGCTGATGGCAGAGCTAACCTGGCCT 3566
QY 269 cccacgagaagatgcaagaggtgacgagagccctggccacacacataagcagagcctg 328
Db 3567 CCCACGAGAAATGACACGAGGCTGACGAGGCTTGGCCACCATTAAGCCAGGCTTG 3626
QY 329 gggagggcaccctctaa 345
Db 3627 GGGAGGGCACCCCTTAA 3643
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RESULT 3
US-08-794-000-3
Sequence 3, Application US/08794000
Patent No. 6087123

GENERAL INFORMATION:
APPLICANT: Metal-Containing Ribonucleotide Polypeptides
TITLE OF INVENTION: Metal-Containing Ribonucleotide Polypeptides
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794.000
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE96/01337
FILING DATE: 17-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 25 992.0
FILING DATE: 17-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 30 500.0
FILING DATE: 18-AUG-1995
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-794-000-3

Query Match 28.6%; Score 98.8; DB 3; Length 273;
Best Local Similarity 63.0%; Pred. No. 5.3e-20;
Matches 170; Conservative 0; Mismatches 97; Indels 3; Gaps 1;

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QY 20 agctggaacgcaacataagacacatcaaaccttcacccaataactctgtggaagctgg 79
Db 5 AGCTGGAGGACCACTGGAGGGCATCATCAACATCTTCCACAGTACTGTGCGGCTGG 64
QY 80 ggcaccagagacacccctgagacacaggggaattcgaacatgagctggtgcgaaagatctgcaaa 139
Db 65 GCCACTATGACACCTGTATCAAGCGGAGCTGTAACACAGCTGATCCAAAGAGAGCTGCCCA 124
QY 140 atttctcaagaagagagaataagaatgaagaagtgatagaacacatcatgagagagctgg 199
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Db 125 ACACCT---GAAGACCAAGACAGGACACCATTTGACAAATCTTCCAGAACTCG 181
Qy 200 acacaatgcaagaagctgagcttcgaagaatcattatgctatgagcgagctaa 259
Db 182 ATGCCAACGAGGATGAGCAGGCTGTCCTTCAAGAGATTGTGTGCTGATCAGATGTGC 241
Qy 260 cctggcctcccaagagaagatgacgagg 289
Db 242 TGATCAGAGCCATGACAAATCCACAAGG 271

RESULT 4
US-08-568-310D-1
; Sequence 1, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568, 310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564(both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PUBLIC INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 1:
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 429
US-08-568-310D-1

Query Match 27.0%; Score 93.2; DB 2; Length 429;
Best Local Similarity 58.8%; Pred. No. 2,9e-18;
Matches 180; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 6 ttgcaaatgctgcagctggaagcaatagacatcatcaaaccttcaccaata 65
Db 41 TGGTAAATGACTAAGCTGAGATCACCTGAGGGAATCATCAATCTCCACCACTA 100
Qy 66 cctctggaagctgggagaccacacccctgacacgaggggaattcaagagctgtg 125

Db 101 CTCGGTTCCGGGTGGGCTATTTCAGACACCTCAACAGCCTGAGCTGAACCTGATC 160
Qy 126 aaaagctgcaaaatttctcaagaagagaaatgaagaagtgatgaacat 185
Db 161 AAGGAACCTCCCAAAACCTCCAGA---ACACCAAGATCAACCTACATTGACAAAT 217
Qy 186 catgagagacttgacaaatgcaagaagcagctgagcttcgaggaattatcatgt 245
Db 218 ATTCCAGAGCTGAGTCCGATTAAGACGAGCGGTGACCTTTGAGGAATTCGTACTCT 277
Qy 246 gatgagagctaacctgggctccacgagaagatgcaagaggtgacgagggccctgg 305
Db 278 GGTGTCAGGGGTCTGAAAACAGCCACATAGATATCCAAAGAGTAGGAAGCTCTTC 337
Qy 306 ccacca 311
Db 338 CAGCAA 343

RESULT 5
US-09-270-455-1
; Sequence 1, Application US/09270455
; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270, 455
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/568, 310
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PUBLIC INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 429
US-09-270-455-1

Query Match 27.0%; Score 93.2; DB 4; Length 429;
Best Local Similarity 58.8%; Pred. No. 2,9e-18;


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;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 12: FROM 1 TO 441
US-09-270-455-12

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Query Match      22.4%; Score 77.4; DB 4; Length 441;
Best Local Similarity 56.8%; Pred. No. 1.2e-13;
Matches 163; Conservative 0; Mismatches 121; Indels 3; Gaps 1;

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QY 3 gacttgcanaagtcgacgtgagagcaacatagagaccatcatcaaaccttcacac 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12 GGTCTGGAGAGTACAAACTTGAAAGCATCTGAGGGAATTTGCAATATCTTCACCA 71
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 atactctgaaagctgggacacacacacacacacacacacacacacacacacacac 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 72 ATACTCAGTTGGAGAGGCGCATTTTGACACCCCTCTTAAGGGTGAAGTGAAGCAGCTGCT 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 123 ggcgaagaagctgcgaatcttcacagaagagatgaatgaatgaatgaatgaatga 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 TACAAGGAGCTTGCAACACATCAAGA--ATATCAAGAATAAAGCTGTCTATTCATCA 188
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 183 calcatggagacgtgacacacacacacacacacacacacacacacacacacac 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 189 AATATTCAGAGGCTGCTGATCTATCAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGA 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 243 gctgatggcgaggtacacacacacacacacacacacacacacacacacacac 289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 249 CCTGTAGCCATTGCGCTGAAGGCTGCCATTACACACACCCACACAAAG 295
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RESULT 8
US-07-662-198B-1
; Sequence 1, Application US/07662198B
; Patent No. 5262528
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; APPLICANT: Lee, Sam W.
; APPLICANT: Tomasello, Catherine
; TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/662,198B
; FILING DATE: 19910228
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/049001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 452
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
US-07-662-198B-1

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Query Match      16.3%; Score 56.2; DB 1; Length 452;
Best Local Similarity 58.0%; Pred. No. 1.9e-07;
Matches 119; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

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QY 47 tcaacaccttcaccaactctctgtgaagctggggaccccaagacacacacacacacac 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 85 TCACCTACCTTCCAAAGACTCTGTCACAGAGGCGCAAGTTCAAGCTTGATGAAGGGGG 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 107 aattcaagagctgtgtggaagaagctgcgaatcttcacagaagaagaagaatga 166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 145 AATTAAGAGAACTTCTGCACAGAGAGCTGCCACCTTTGT--GGGGAGAGAAAGTGATG 201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 167 aaaaagtcatagaacacacacacacacacacacacacacacacacacacacac 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 202 AGGAGGCGCTGCAAGAGCTGATGGGCAACCTGATGAGACAGTGAACCAAGTGAAGTGA 261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 227 tcgagagcttcacatgctgctgac 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 262 TCAGAGAGATGCTGTTTCTCTGCC 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 9
US-08-322-742-1
; Sequence 1, Application US/08322742
; Patent No. 5688641
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/322,742
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: September 1, 1992
; APPLICATION NUMBER: 07/844,296
; FILING DATE: February 28, 1992
; APPLICATION NUMBER: 07/552,216
; FILING DATE: February 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/048003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-322-742-1

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Query Match 16.3%; Score 56.2; DB 1; Length 452;
Best Local Similarity 58.0%; Pred. No. 1.9e-07;
Matches 119; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

QY 47 tcaaaccttcacacatactctgtgaagctggtggcaccacacacccctgaacccagggg 106
DB 85 TCACACTCTCCACAACTACCTCCCAAGAGGCGACACAGTTCACAGCTGAGTAAAGGGG 144
QY 107 aattcaagagctggtgggaaaaagctgcgaattttctcaagaagagagataagatg 166
DB 145 AATGAGAGACTCTGTGACAAAGAGGCTGCCAGCTTGT--GGGGGAAAGTGGATG 201
QY 167 aaaaagtcataagacacacatcatgagagacctgtgacacacaaatgcagacaagcgtgagct 226
DB 202 AGGAGGGGCTGAAGAAGCTGATGGGCAACCTGATGACAAACAGTACACAGAGGAGTGCAC 261
QY 227 tcgagagctcatalcgtctgtaggc 251
DB 262 TCCAGGAGTATGCTGTCTTCTGCGC 286

RESULT 10

US-08-190-560-3
Sequence 3, Application US/08190560
Patent No. 5798257
GENERAL INFORMATION:
APPLICANT: Zain, Sayeeda
APPLICANT: Lukanidin, Eugene
TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
TITLE OF INVENTION: THE MTS-1 GENE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,560
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 78792Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-190-560-3

Query Match 13.6%; Score 47; DB 1; Length 579;
Best Local Similarity 50.9%; Pred. No. 0.00011;
Matches 138; Conservative 0; Mismatches 130; Indels 3; Gaps 1;
QY 5 ctgtgaaatgtcgcagctgtgaagcacaatagagacatcatcaaaccttcacacaat 64
DB 131 CTGTGATGCGGTGCCCTGTGAGAGGCCCTGATGTGATGTCTCCACCTTCACAGAT 190

DB 131 CTGTGATGCGGTGCCCTGTGAGAGGCCCTGATGTGATGTCTCCACCTTCACAGAT 190
QY 65 actctgtgaagctgtgggacccacacacccctgaacccagggggaattcaagagctgtgc 124
DB 191 ACTCGGCAAGAGGGGTACAAAGTTCAAGCTCAACAAAGTCAAGAACTAAAGAGCTCTGA 250
QY 125 gaaaagatctgaaattttctcaagaaggaataaagaatgaagaagtcataagacaa 184
DB 251 CCCGGAGACTGCGCCAGCTTCTTGGGAAAGACAG--ATGAAGCTGCTTCCAGAGC 307
QY 185 tcatgagagactgtgacacaaatgcagacagcagctgcgttcgtgagagctcatalgc 244
DB 308 TATATGACAACCTTGACGACCAACAGGCAACAGAGGTGAGACTTCCAAAGACTGTGTCT 367
QY 245 tcatgagagctgaacctgtgagcctccacga 275
DB 368 TCTCTGCTGATGCGCATGATGTGTAAAGCA 398

RESULT 11

US-08-469-277-3
Sequence 3, Application US/08469277
Patent No. 580142
GENERAL INFORMATION:
APPLICANT: Zain, Sayeeda
APPLICANT: Lukanidin, Eugene
TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
TITLE OF INVENTION: THE MTS-1 GENE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,277
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/190,560
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 78792Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-469-277-3

Query Match 13.6%; Score 47; DB 1; Length 579;
Best Local Similarity 50.9%; Pred. No. 0.00011;
Matches 138; Conservative 0; Mismatches 130; Indels 3; Gaps 1;
QY 5 ctgtgaaatgtcgcagctgtgaagcacaatagagacatcatcaaaccttcacacaat 64
DB 131 CTGTGATGCGGTGCCCTGTGAGAGGCCCTGATGTGATGTCTCCACCTTCACAGAT 190

Oy	65	actctgtggaagcttggggcagcccagacacccctgaaacccagggggaattcaaaagactgtgtgc	124
Db	191	actggggcacaagaggggtgacactgttcaactcaaccaagtacgaactaaaggagctgtga	250
Oy	125	gaaagaatctgcaaatcttctcagaagaagaaatgaagtgaagaagtcataagaacaa	184
Db	251	ccccggagctccccaagcttcttgggggaaaaagaaag---atgaagctgcgtttccagaagc	307
Oy	185	tcatgtgaagaccttggacacaacaatgacagacaagacagctgagcttcagaaagttcaatc	244
Db	308	tgatgacgaacacttggacagcacaacagggacaacagagtggaacttccaaagactagtgtct	367
Oy	245	tgatgtgcgaagctaaccttgggcccctccacga	275
Db	368	ttctctgtccctgcattgcccatgtatgtgtgaacga	398

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12
US-08-468-946-3
; Sequence 3, Application US/08468946
; Patent No. 5843686
; GENERAL INFORMATION:
; APPLICANT: Zain, Sayeeda
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; TITLE OF INVENTION: THE MTS-1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,946
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,560
; FILING DATE: 31-JAN-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 78792Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; TELEX: 230 901 SANS UR
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
;
; US-08-468-946-3

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Query Match	13.6%	Score 47	DB 2:	Length 579:
Best Local Similarity	50.9%	Pred No. 0.0011:		
Matches 138:	Conservative	0;	Mismatches 130:	Indels 3;
				Gaps 1
QY	5	cttgcgaatatgtcgcagctgtggaacgcacaatagagacatcatcaacaccttccaccaat	64	
Db	131	CGTCATGCGCGCCCTTCGGAGAACGCCCTCGATGTGATGGTGTCCACCTTCCACAAGT	190	

Qy	65	actctgtgaagctctgggagaccagacacccctggaacccaggggaattcaagaagctgtg	124
Db	191	ACTCGGGCAAGAGAGGGGTGACAAAGTTCACAGCTCAACAGTCAAGACTAAAGAGCTGCTGA	250
Qy	125	gaaaagatctgcaaaattttctcagaagaaggaataaagaatgaaagatcatagaacaca	184
Db	251	CCCGGAGCTCTCCCAAGCTTTCTTGGGGAAAAAGGACAG--ATGAAGCTTCGTTCCAGAAAGC	307
Qy	185	tcatggaagaccctggacacaaatgcagacaagaacgcttgagctctgaggaagtcatatgc	244
Db	308	TGATAGGCAACCTTGAGACAGCAACAGGGGCAACAGAGGTGAGACTTCCAAAGAGTACTGTGCT	367
Qy	245	tgatggagagcttaaacctcgggcctccacga	275
Db	368	TCTCTCTCTGCATCGCCATGTATGTATAACA	398

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13
US-08-468-942-3
: Sequence 3, Application US/08468942
: Patent No. 5965360
: GENERAL INFORMATION:
: APPLICANT: Zain, Sayeeda
: APPLICANT: Lukanidin, Eugene
: TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
: TITLE OF INVENTION: THE MTS-1 GENE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
: STREET: 400 Garden City Plaza
: CITY: Garden City
: STATE: New York
: COUNTRY: United States
: ZIP: 11530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/468,942
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/190,560
: FILING DATE: 31-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Digiglio, Frank S.
: REGISTRATION NUMBER: 31,346
: REFERENCE/DOCKET NUMBER: 78792Y
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (516) 742-4343
: TELEFAX: (516) 742-4366
: TELEX: 230 901 SANS UR
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 579 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
US-08-468-942-3

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Query Match	13.6%	Score 47	DB 2	Length 579
Best Local Similarity	50.9%	Pred. No. 0.00011		
Matches 138	Conservative	0	Mismatches 130	Indels 3
				Gaps 1
QY	5	cttgcgaatgtcgcagctgggaacgaatagagacccttcaaaccttccaccat	64	
Db	131	ctgtctatggcggctccctcttgcgaacagcccttgatattgattgctgcacccttccacaaatt	190	
QY	65	actctgtgaagctgtgggacacccagacacccctgaaccagtggaattcaagaagctgtgtgc	124	

Db 2387 CACCTGGACCCCGGTGAGCAGTGCAGTGCCTCCCTCCCTCCGCGGGGAGGCACT 2446
Qy 198 g 198
Db 2447 G 2447

Search completed: September 10, 2002, 06:44:15
Job time: 4961 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 06:49:27 : Search time 298.43 Seconds
(without alignments)
1984.839 Million cell updates/sec

Title: US-09-806-382A-2
Perfect score: 345
Sequence: 1 atgacttgcaaaatgtcgca.....tcggggagggcaccctctaa 345

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
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23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345	100.0	345	21 AAC81809	Human S100A9 cDNA.
2	345	100.0	345	21 AA11970	Human calcium-bind
3	345	100.0	565	22 AAF54714	Nucleotide sequenc
4	345	100.0	565	22 AAF54719	Nucleotide sequenc
5	345	100.0	571	19 AA134698	Human calprotectin
6	345	100.0	687	20 AA233673	Human breast tumou
7	345	100.0	688	20 AA233615	Human breast tumou
8	345	100.0	771	22 AA159150	Human polynucleoti
9	267.4	77.5	452	22 AAF54717	Nucleotide sequenc

10	262.2	76.0	342	22 AAF54709	Nucleotide sequenc
11	261.6	75.8	345	21 AA160936	Human polynucleoti
12	260.2	75.4	385	21 AAC06727	Human secreted pro
13	242	70.1	430	22 AAF54715	Nucleotide sequenc
14	241	69.9	425	22 AAF54713	Nucleotide sequenc
15	197	57.1	592	22 ABA59810	Human foetal liver
16	197	57.1	592	22 ABA28288	Probe #6754 for ge
17	197	57.1	592	22 AAK08083	Human brain expres
18	197	57.1	592	22 AAK33958	Human bone marrow
19	197	57.1	592	22 AA116584	Probe #6517 for ge
20	197	57.1	592	22 AA139682	Probe #8368 used t
21	197	57.1	4439	22 AAF54718	Nucleotide sequenc
22	197	57.1	4440	18 AAT68322	Human multitrug re
23	195	56.5	195	22 ABA72351	Human foetal liver
24	195	56.5	195	22 ABA38167	Probe #16633 for g
25	195	56.5	195	22 AAK20777	Human brain expres
26	195	56.5	195	22 AAK46926	Human bone marrow
27	195	56.5	195	22 AA125780	Probe #15713 for g
28	195	56.5	195	22 AA152763	Probe #21449 used
29	181.6	52.6	406	22 AAF54712	Nucleotide sequenc
30	177.4	51.4	350	20 AAX23464	Human neutrophil c
31	150	43.5	594	22 ABA61147	Human foetal liver
32	150	43.5	594	22 ABA29027	Probe #7493 for ge
33	150	43.5	594	22 AAK09442	Human brain expres
34	150	43.5	594	22 AAK35334	Human bone marrow
35	150	43.5	594	22 AA116996	Probe #6929 for ge
36	150	43.5	594	22 AA141047	Probe #9733 used t
37	133	38.6	133	22 ABA73673	Human foetal liver
38	133	38.6	133	22 ABA38897	Probe #17363 for g
39	133	38.6	133	22 AAK22120	Human brain expres
40	133	38.6	133	22 AAK48287	Human bone marrow
41	133	38.6	133	22 AA126189	Probe #16122 for g
42	133	38.6	133	22 AA154112	Probe #22798 used
43	109.6	31.8	477	22 AAF54711	Nucleotide sequenc
44	109	31.6	305	22 AAF54716	Nucleotide sequenc
45	103.2	29.9	347	23 AAS96258	Human bone marrow

ALIGNMENTS

RESULT 1	
ID AAC81809	standard; cDNA; 345 BP.
XX	
XX AAC81809;	
XX	
DT 22-FEB-2001	(first entry)
XX	
DE Human S100A9 cDNA.	
XX	
KW S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;	
KW calcium-binding protein; calcium homeostasis; cardiac muscle;	
KW pumping capacity; myocardial cell; systolic calcium ion release;	
KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;	
KW valve defect; ss.	
XX	
OS Homo sapiens.	
XX	
PN DE19915485-A1.	
XX	
PD 19-OCT-2000.	
XX	
PF 07-APR-1999;	99DE-1015485.
XX	
PR 07-APR-1999;	99DE-1015485.
XX	
PA (KATU/) KATUS H A.	
XX (REMP/) REMPPIS A.	
XX	
PI Katus HA, Remppis A;	
XX	
DR WPI; 2000-673510/66.	

DR P-PSDB: AAB45539.
XX Composition containing S100 protein, corresponding nucleic acid or
PT vector, useful for treating cardiomyopathy and cardiac insufficiency -
XX
PS Claim 36; Page 16; 36pp; German.
XX
CC This invention describes a novel composition for treating primary or
CC secondary cardiomyopathy or cardiac insufficiency contains at least one
CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
CC fragments, or a gene transfer vector containing (II), optionally
CC formulated with auxilliaries and/or carriers. (I) are calcium-binding
CC proteins involved in calcium homeostasis, so their overexpression in
CC cardiac muscle will improve pumping capacity (and overall contraction) of
CC the heart. In cultured myocardial cells they increase the contraction and
CC relaxation rates associated with increased systolic calcium ion release
CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
CC used to treat cardiomyopathy (CMP) where inherited or caused by
CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
CC by pulmonary and/or arterial hypertension, and structural disease caused
CC by rhythm disorders or valve defects, generally any condition associated
CC with reduced contractile force. Unlike calmodulin, which is expressed
CC ubiquitously, (I) show tissue-specific expression and treat the
CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
CC disease.
XX
SQ Sequence 345 BP; 110 A; 89 C; 92 G; 54 T; 0 other;
XX
Query Match 100.0%; Score 345; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 atgcttgcacaaatgtcgcagctggaagcgaacatagagacatcatcaaccccttcac 60
DB 1 atgacttgcacaaatgtcgcagctggaagcgaacatagagacatcatcaaccccttcac 60
QY 61 caatactctgtgaagcttgcgcacccacagacccctgaaccagggggaattcaaaagctg 120
DB 61 caatactctgtgaagcttgcgcacccacagacccctgaaccagggggaattcaaaagctg 120
QY 121 gtgcgaaaagatctgcacaaatttctcaagaagagaataagatgaagaagtcatagaa 180
DB 121 gtgcgaaaagatctgcacaaatttctcaagaagagaataagatgaagaagtcatagaa 180
QY 181 cacatcatgagagaccttgcacacaaatgcagacagcgtgagcttcgaggagttcattc 240
DB 181 cacatcatgagagaccttgcacacaaatgcagacagcgtgagcttcgaggagttcattc 240
QY 241 atgctgatgagagctaaccttgcgcctccacagagaagatgcacgaggtgcagagggc 300
DB 241 atgctgatgagagctaaccttgcgcctccacagagaagatgcacgaggtgcagagggc 300
QY 301 cctggccacccacataagccagcgtctcgggagggcaccccttaa 345
DB 301 cctggccacccacataagccagcgtctcgggagggcaccccttaa 345
XX
RESULT 2
AA11970
ID AA11970 standard; DNA: 345 BP.
XX
AC AA11970;
XX
XX 04-AUG-2000 (first entry)
DE Human calcium-binding protein encoding DNA #2.
XX
XX Calcium-binding protein; granule release; calgranulin; human;
KW vascular membrane growth; adult respiratory distress syndrome;
KM acute myocardial infarction; ischemic reperfusion disorder;
KM glomerulonephritis; rheumatoid arthritis; chronic bronchitis;

KW cerebral vascular disorder; asthma; peripheral circulation disturbance;
KM angina pectoris; hypertension; multiple sclerosis; ds.
XX
XX Homo sapiens.
XX
XX WO200018970-A1.
XX
XX PD 06-APR-2000.
XX
XX PF 28-SEP-1999; 99WO-JP05302.
XX
XX PR 29-SEP-1998; 98JP-0274574.
XX
XX PA (ASAH) ASAMI KASEI KOGYO KK.
XX
XX Seto M, Fukuda K;
PI
XX WPI; 2000-293189/25.
DR P-PSDB: AAV87637.
XX
XX Controlling the release of granules from cell system using activated
PT calgranulin for screening substances for granule activating or
PT inhibiting activity -
PS Claim 3(11); Page 39-40; 42pp; Japanese.
XX
CC This invention describes a novel method for controlling the release of
CC granules by treating a cell system to increase or decrease activated
CC calgranulin to enhance or depress the release of granules. Calgranulin
CC is a calcium binding protein and can be used for controlling the release
CC of granules from a cell system e.g. those involved with the inhibition of
CC vascular membrane growth. Vascular membrane growth is associated with
CC e.g. adult respiratory distress syndrome, acute myocardial infarction due
CC to ischemic reperfusion disorders, glomerulonephritis, rheumatoid
CC arthritis, chronic bronchitis, cerebral vascular disorders, asthma,
CC peripheral circulation disturbance, angina pectoris, hypertension and
CC multiple sclerosis. The new method is used for screening substances for
CC their ability to activate or inhibit the release of granules. This
CC sequence encodes a human calcium-binding protein which is described in
CC the method of the invention.
XX
SQ Sequence 345 BP; 110 A; 89 C; 92 G; 54 T; 0 other;
XX
Query Match 100.0%; Score 345; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 atgacttgcacaaatgtcgcagctggaagcgaacatagagacatcatcaaccccttcac 60
DB 1 atgacttgcacaaatgtcgcagctggaagcgaacatagagacatcatcaaccccttcac 60
QY 61 caatactctgtgaagcttgcgcacccacagacccctgaaccagggggaattcaaaagctg 120
DB 61 caatactctgtgaagcttgcgcacccacagacccctgaaccagggggaattcaaaagctg 120
QY 121 gtgcgaaaagatctgcacaaatttctcaagaagagaataagatgaagaagtcatagaa 180
DB 121 gtgcgaaaagatctgcacaaatttctcaagaagagaataagatgaagaagtcatagaa 180
QY 181 cacatcatgagagaccttgcacacaaatgcagacagcgtgagcttcgaggagttcattc 240
DB 181 cacatcatgagagaccttgcacacaaatgcagacagcgtgagcttcgaggagttcattc 240
QY 241 atgctgatgagagctaaccttgcgcctccacagagaagatgcacgaggtgcagagggc 300
DB 241 atgctgatgagagctaaccttgcgcctccacagagaagatgcacgaggtgcagagggc 300
QY 301 cctggccacccacataagccagcgtctcgggagggcaccccttaa 345
DB 301 cctggccacccacataagccagcgtctcgggagggcaccccttaa 345


```
RESULT 3
AAF54714
ID AAF54714 standard; DNA; 565 BP.
XX
AC AAF54714;
XX
DT 15-MAY-2001 (first entry)
XX
DE Nucleotide sequence of a human polynucleotide sequence.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-FR02057.
XX
PR 15-JUL-1999; 99FR-0009372.
XX
PA (INMR ) BIOMERIEUX STELHYS.
XX
PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX
DR WPI: 2001-159475/16.
XX
PT Detecting, preventing and treating degenerative, neurological and
XX autoimmune diseases, particularly multiple sclerosis, using specified
XX polypeptides or related nucleic acid or ligand -
XX
PS Claim 11; Page 186; 209pp; French.
XX
CC The present sequence represents a human polynucleotide sequence, which
CC is used in the method of the invention. The specification describes a
CC method which uses at least one polypeptide or polynucleotide sequence
CC belonging to the perlecan, precursor of the retinol-binding plasma
CC protein, precursor of the ganglioside GM2 activator, calgranulin B or
CC saposin B protein families. The method is used for detecting,
CC preventing or treating a degenerative, neurological and/or auto-immune
CC disease. The polynucleotides and polypeptides are used for diagnosis,
CC prognosis, prevention and treatment of multiple sclerosis (in its
CC various forms and phases). They may also be useful in cases of
CC e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis,
CC Rheumatoid polyarthritis and lupus erythematosus, including use as
CC vaccines and in gene therapy (expression of sense or antisense
CC sequences). They can also be used to assess efficacy of potential
CC therapeutic agents, particularly compounds that reduce or inhibit
CC toxicity towards glial cells.
XX
SQ Sequence 565 BP; 158 A; 158 C; 156 G; 93 T; 0 other;

Query Match 100.0%; Score 345; DB 22; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgacttgtaaatgtcgagctggaacgacaatagagaccatcatcaacaccttccac 60
DB ||||||
32 atgacttgtaaatgtcgagctggaacgacaatagagaccatcatcaacaccttccac 91
QY 61 caatactctgtgaagctggggcaccagacacccctgaaccagggggaattcaagaagctg 120
DB ||||||
92 caatactctgtgaagctggggcaccagacacccctgaaccagggggaattcaagaagctg 151
QY 121 gtgcgaaagaatctgcaaatcttctcaagaagagagaatgaatgaagaagctataga 180
DB ||||||
152 gtgcgaaagaatctgcaaatcttctcaagaagagagaatgaatgaagaagctataga 211
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QY 181 cacatcatgagagacctgagcacacaatgacagaacgagctgagcttcgaagatcatc 240
DB ||||||
212 cacatcatgagagacctgagcacacaatgacagaacgagctgagcttcgaagatcatc 271
QY 241 atgctgatggcagagcttaacctggcctccacagaagaatgacagaggtgacagagac 300
DB ||||||
272 atgctgatggcagagcttaacctggcctccacagaagaatgacagaggtgacagagac 331
QY 301 cctggcaccaccataagcagagcctcgaggagagcccccctaa 345
DB ||||||
332 cctggcaccaccataagcagagcctcgaggagagcccccctaa 376

RESULT 4
AAF54719
ID AAF54719 standard; DNA; 565 BP.
XX
AC AAF54719;
XX
DT 15-MAY-2001 (first entry)
XX
DE Nucleotide sequence of a human polynucleotide sequence.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-FR02057.
XX
PR 15-JUL-1999; 99FR-0009372.
XX
PA (INMR ) BIOMERIEUX STELHYS.
XX
PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX
DR WPI: 2001-159475/16.
XX
PT Detecting, preventing and treating degenerative, neurological and
XX autoimmune diseases, particularly multiple sclerosis, using specified
XX polypeptides or related nucleic acid or ligand -
XX
PS Claim 11; Page 188; 209pp; French.
XX
CC The present sequence represents a human polynucleotide sequence, which
CC is used in the method of the invention. The specification describes a
CC method which uses at least one polypeptide or polynucleotide sequence
CC belonging to the perlecan, precursor of the retinol-binding plasma
CC protein, precursor of the ganglioside GM2 activator, calgranulin B or
CC saposin B protein families. The method is used for detecting,
CC preventing or treating a degenerative, neurological and/or auto-immune
CC disease. The polynucleotides and polypeptides are used for diagnosis,
CC prognosis, prevention and treatment of multiple sclerosis (in its
CC various forms and phases). They may also be useful in cases of
CC e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis,
CC Rheumatoid polyarthritis and lupus erythematosus, including use as
CC vaccines and in gene therapy (expression of sense or antisense
CC sequences). They can also be used to assess efficacy of potential
CC therapeutic agents, particularly compounds that reduce or inhibit
CC toxicity towards glial cells.
XX
SQ Sequence 565 BP; 158 A; 158 C; 156 G; 93 T; 0 other;

Query Match 100.0%; Score 345; DB 22; Length 565;
```

```
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 32 atgacttgcaaaatgtcgagctggaacgcaacatagagacatctcaacacctccac 91
QY 61 caatactctgttaaagctgggacaccacacctgaaccagggggaattcaaaagctg 120
DB 92 caatactctgttaaagctgggacaccacacctgaaccagggggaattcaaaagctg 151
QY 121 gtgcgaaaaagatctgcaaaattttctcaagaaggagaataaagaatgcatagaa 180
DB 152 gtgcgaaaaagatctgcaaaattttctcaagaaggagaataaagaatgcatagaa 211
QY 181 caacatcagagagctggaacacaaatgagacaagcaagctgagcttgaggagttcacc 240
DB 212 caacatcagagagagctggaacacaaatgagacaagcaagctgagcttgaggagttcacc 271
QY 241 atgctgatatggcgaggttaaacctgggcctccacagagaagaatcacagaggtgacgagggc 300
DB 272 atgctgatatggcgaggttaaacctgggcctccacagagaagaatcacagaggtgacgagggc 331
QY 301 cctggcaccaccacataaagcgaagcctcggggaggggacccctctaa 345
DB 332 cctggcaccaccacataaagcgaagcctcggggaggggacccctctaa 376

RESULT 5
AAV34698
ID AAV34698 standard; cDNA: 571 BP.
AC AAV34698;
XX
XX 03-SEP-1998 (first entry)
DT
XX Human calprotectin subunit MRP-14 protein encoding cDNA.
DE
XX Human; MRP-8; MRP-14; calprotectin; mineral precipitate; struvite;
KW calcium phosphate; kidney stone; renal calculi; struvite stone;
XX urinary tract infection; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 44..385
XX FT /*tag= a
XX FT /product= "human MRP-14"
XX
XX US5776348-A.
XX
XX 07-JUL-1998.
XX
XX 07-FEB-1995; 95US-0385241.
XX
XX 07-FEB-1995; 95US-0385241.
XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Asakura H, Dretler SP, Orme-johnson WH, Selengut JD;
XX WPI; 1998-397914/34.
XX
XX P-PSDB; AAM60178.
XX
XX Inhibiting kidney stone formation - uses the protein calprotectin
XX
XX Example 1; Columns 23-24; 19pp; English.
XX
XX This cDNA encodes a human calprotectin subunit MRP-14. This is used in
XX a method for inhibiting the formation of a mineral precipitate in a
XX solution which comprises providing a solution comprising component ions
XX of the mineral precipitate or its precursors and contacting the solution
XX with an effective amount of isolated calprotectin, or a derivative of it.
XX
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CC The method is useful for the inhibition of kidney stone formation (renal
CC calculi). Kidney stones are concentrations of inorganic and organic salts
CC that develop though crystal nucleation, aggregation and growth in the
CC kidneys, which then can block the urether and if not passed to the
CC bladder, grow and become symptomatic. Struvite stones (MgNH4PO4) are
CC commonly found after urinary tract infection. The mechanisms of this and
CC other stone formation is unclear, but some urine compositions are known
CC to inhibit formation. One of the major components of these is a protein
CC factor calprotectin, which inhibits mineral precipitation. Calprotectin
CC can also be used to raise antibodies, which in turn can be used to detect
CC the protein in samples. The levels of calprotectin found in samples can
CC be compared to levels found in normal humans, and thus assuming increased
CC calprotectin correlates to indication of kidney stone formation, this
CC procedure can be used as a diagnostic tool.
XX
SQ Sequence 571 BP; 160 A; 160 C; 157 G; 94 T; 0 other;

Query Match 100.0%; Score 345; DB 19; Length 571;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 caatactctgttaaagctgggacaccacacctgaaccagggggaattcaaaagctg 120
DB 104 caatactctgttaaagctgggacaccacacctgaaccagggggaattcaaaagctg 163
QY 121 gtgcgaaaaagatctgcaaaattttctcaagaaggagaataaagaatgcatagaa 180
DB 164 gtgcgaaaaagatctgcaaaattttctcaagaaggagaataaagaatgcatagaa 223
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DB 224 caacatcagagagagctggaacacaaatgagacaagcaagctgagcttgaggagttcacc 283
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DB 344 cctggcaccaccacataaagcgaagcctcggggaggggacccctctaa 388

RESULT 6
AAZ33673
ID AAZ33673 standard; cDNA: 687 BP.
AC AAZ33673;
XX
XX 08-DEC-1999 (first entry)
DT
XX Human breast tumour-associated EST 63.
DE
XX Expressed sequence tag; EST; human; breast; cancer; gene therapy;
XX treatment; tumour; cytostatic; medicament; ss.
XX
XX Homo sapiens.
XX
XX DE19813839-A1.
XX
XX 23-SEP-1999.
XX
XX 20-MAR-1998; 98DE-1013839.
XX
XX 20-MAR-1998; 98DE-1013839.
XX
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX
```

XX WPI: 1999-528981/45.
DR P-PSDB: AAY48615.
XX Human nucleic acid sequences and protein products from tumor breast
PT tissue, useful for breast cancer therapy -
XX Claim 3; 141; 188bp; German.
XX
CC This invention describes novel human nucleic acid sequences from tumor
CC breast tissue which have cytoskeletal activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can
CC be used to express proteins, which can be used as tools to find an
CC actively against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medications for gene
CC therapy to treat breast cancer. AA233611-248617 represents expressed
CC sequence tags described in the method of the invention.
XX
SQ Sequence 687 BP; 177 A; 198 C; 190 G; 122 T; 0 other;

Query Match 100.0%; Score 345; DB 20; Length 687;

Best Local Similarity 100.0%; Pred. No. 2.7e-86;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgactgtcaaaatgtcgcagctggaacgcaacatagagaccatcatcaacaccttcac 60
DB 101 atgactgtcaaaatgtcgcagctggaacgcaacatagagaccatcatcaacaccttcac 160
OY 61 caatactctgtgaagctgtgggacccagacacacctgtgaaccagggggaattcaagaagctg 120
DB 161 caatactctgtgaagctgtgggacccagacacacctgtgaaccagggggaattcaagaagctg 220
OY 121 gtgcgaaaagatctgcacaaatttctcaagaaggagataagaatgataaaggtcatagaa 180
DB 221 gtgcgaaaagatctgcacaaatttctcaagaaggagataagaatgataaaggtcatagaa 280
OY 221 gtgcgaaaagatctgcacaaatttctcaagaaggagataagaatgataaaggtcatagaa 280
DB 281 cacatcatgtgagacctgtgacacaaatgacagcaagcgtgagcttcgagagatcatc 340
OY 181 cacatcatgtgagacctgtgacacaaatgacagcaagcgtgagcttcgagagatcatc 240
DB 281 cacatcatgtgagacctgtgacacaaatgacagcaagcgtgagcttcgagagatcatc 340
OY 241 atgctgtagtggaagctaacctgtggtctccacgagaagaatgacagaggtgacgagggc 300
DB 341 atgctgtagtggaagctaacctgtggtctccacgagaagaatgacagaggtgacgagggc 400
OY 301 cctggcaccaccataagccagcctcggggagggcaccacctaa 345
DB 401 cctggcaccaccataagccagcctcggggagggcaccacctaa 445

RESULT 7

AA233615
ID AA233615 standard; cDNA; 688 BP.

XX AA233615;

XX 08-DEC-1999 (first entry)

XX Human breast tumour-associated EST 5.

XX Expressed sequence tag; EST; human; breast; cancer; gene therapy;
KW treatment; tumour; cytoskeletal; medication; ss.

XX Homo sapiens.

XX DE19813839-A1.

XX 23-SEP-1999.

XX 20-MAR-1998; 98DE-1013839.

XX 20-MAR-1998; 98DE-1013839.

XX PR

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX Specht T, Hinemann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX WPI: 1999-528981/45.
XX Human nucleic acid sequences and protein products from tumor breast
PT tissue, useful for breast cancer therapy -
XX Claim 3; 86; 188bp; German.
XX
CC This invention describes novel human nucleic acid sequences from tumor
CC breast tissue which have cytoskeletal activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can
CC be used to express proteins, which can be used as tools to find an
CC actively against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medications for gene
CC therapy to treat breast cancer. AA233611-248617 represents expressed
CC sequence tags described in the method of the invention.
XX
SQ Sequence 688 BP; 178 A; 198 C; 190 G; 122 T; 0 other;

Query Match 100.0%; Score 345; DB 20; Length 688;

Best Local Similarity 100.0%; Pred. No. 2.7e-86;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgactgtcaaaatgtcgcagctggaacgcaacatagagaccatcatcaacaccttcac 60
DB 101 atgactgtcaaaatgtcgcagctggaacgcaacatagagaccatcatcaacaccttcac 160
OY 61 caatactctgtgaagctgtgggacccagacacacctgtgaaccagggggaattcaagaagctg 120
DB 161 caatactctgtgaagctgtgggacccagacacacctgtgaaccagggggaattcaagaagctg 220
OY 121 gtgcgaaaagatctgcacaaatttctcaagaaggagataagaatgataaaggtcatagaa 180
DB 221 gtgcgaaaagatctgcacaaatttctcaagaaggagataagaatgataaaggtcatagaa 280
OY 221 gtgcgaaaagatctgcacaaatttctcaagaaggagataagaatgataaaggtcatagaa 280
DB 281 cacatcatgtgagacctgtgacacaaatgacagcaagcgtgagcttcgagagatcatc 340
OY 181 cacatcatgtgagacctgtgacacaaatgacagcaagcgtgagcttcgagagatcatc 240
DB 281 cacatcatgtgagacctgtgacacaaatgacagcaagcgtgagcttcgagagatcatc 340
OY 241 atgctgtagtggaagctaacctgtggtctccacgagaagaatgacagaggtgacgagggc 300
DB 341 atgctgtagtggaagctaacctgtggtctccacgagaagaatgacagaggtgacgagggc 400
OY 301 cctggcaccaccataagccagcctcggggagggcaccacctaa 345
DB 401 cctggcaccaccataagccagcctcggggagggcaccacctaa 445

RESULT 8

AA159150
ID AA159150 standard; cDNA; 771 BP.

XX AA159150;

XX 22-OCT-2001 (first entry)

XX Human polynucleotide SEQ ID NO 1353.

XX Human; neotropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.

XX Homo sapiens.

XX 20-MAR-1998; 98DE-1013839.

XX 20-MAR-1998; 98DE-1013839.

XX PR

XX W0200153312-A1.

Db	418	ccggccaccacacataagccagcgtcgaggagggacccctaa	462
RESULT	9		
AAF54717/c			
ID	AAF54717	standard; DNA: 452 BP.	
XX			
AAF54717;			
XX			
DT	15-MAY-2001	(first entry)	
XX			
DE		Nucleotide sequence of a human polynucleotide sequence.	
XX			
Human: perlecan: retinol-binding plasma protein; calgranulin B; vaccine;			
KW	ganglioside GM2 activator; saposin B; degenerative disease; glial cell;		
KW	neurological disease; auto-immune disease; multiple sclerosis; toxicity;		
KW	Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;		
XX	rheumatoid polyarthritits; lupus erythematosus; gene therapy; ss.		
OS	Homo sapiens.		
XX			
PN	MO200105422-AZ.		
XX			
PD	25-JAN-2001.		
XX			
PF	17-JUL-2000; 2000MO-FR02057.		
XX			
PR	15-JUL-1999; 99FR-0009372.		
XX			
PA	(INMR) BIOMERIEUX STELMYS.		
XX			
PI	Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;		
XX	WPI: 2001-159475/16.		
DR			
XX		Detecting, preventing and treating degenerative, neurological and	
PT	autoimmune diseases, particularly multiple sclerosis, using specified		
PT	polypeptides or related nucleic acid or ligand		
XX			
PS	Claim 11: Page 186-187; 209pp; French.		
XX			
CC	The present sequence represents a human polynucleotide sequence, which		
CC	is used in the method of the invention. The specification describes a		
CC	method which uses at least one polypeptide or polynucleotide sequence		
CC	belonging to the perlecan, precursor of the retinol-binding plasma		
CC	protein, precursor of the ganglioside GM2 activator, calgranulin B or		
CC	saposin B protein families. The method is used for detecting,		
CC	preventing or treating a degenerative, neurological and/or auto-immune		
CC	disease. The polynucleotides and polypeptides are used for diagnosis,		
CC	prognosis, prevention and treatment of multiple sclerosis (in its		
CC	various forms and phases). They may also be useful in cases of		
CC	e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis,		
CC	rheumatoid polyarthritits and lupus erythematosus, including use as		
CC	vaccines and in gene therapy (expression of sense or antisense		
CC	sequences). They can also be used to assess efficacy of potential		
CC	therapeutic agents, particularly compounds that reduce or inhibit		
CC	toxicity towards glial cells.		
XX			
Sequence	452 BP; 69 A; 131 C; 129 G; 123 T; 0 other;		
Query Match	77.5%; Score 267.4; DB 22; Length 452;		
Best Local Similarity	99.6%; Pred. No. 9,1e-65;		
Matches 268; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
77	tcggggaccacacaccccggaaccgagggggaattcaaaagactgtgtcgaaaagattcgc	136	
DB	452 TGGGGCACCCAGACCCCTGAACGAGGGGGAATTCAAGAGCTGGTGGGAAAGATCTGC	393	
77	aaaatttctcaagaagagaataaagaatgaagaagtcattatagaacacatcgtgagacc	196	
DB	392 AAAATTTTCTCAGAAGAGGAATTAAGATGAAAAGTGATAGAACATCATCATGAGGACC	333	

QY 197 tgcacacaaatgcagacagcagctgcgcgaggaatcatatcgtatgcgagcgc 256
|||||
DB 332 TGGACACAAATGACAGACAGCTGCAGAGATTTCATCATGCTGATGCGAGGC 273
QY 257 taactggtgctcccaagagaagatgcaggggtgacgagggccctggccaccacata 316
|||||
DB 272 TAACCTGGGCTCCACAGCAAAATGCACGAGGTTGACGAGGGCCCTGGCCACACACATA 213
QY 317 agccagagctcgaggagggaccccccctaa 345
|||||
DB 212 AGCCAGGCTCGGGAGGCGCACCCCTTA 184

RESULT 10
AAFS4709
ID AAF54709 standard; DNA; 342 BP.
XX
AC AAF54709;
XX
DT 15-MAY-2001 (first entry)
XX
DE Nucleotide sequence of precursor of retinol-binding plasma protein.
XX
XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KM ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KM neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KM Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KM rheumatoid polyarthritis; lupus erythematosus; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PE 17-JUL-2000; 2000WO-FR02057.
XX
PR 15-JUL-1999; 99FR-0009372.
XX
XX (INMR) BIOMERIEUX STELHYS.
XX
PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX WPI: 2001-159475/16.
XX P-PSDB: AAB31905.
XX
DR Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand -
XX
XX
PS Claim 11; Page 183; 209pp; French.
XX
XX The present sequence represents a human polynucleotide, which is used
CC in the method of the invention. The specification describes a method
CC which uses at least one polypeptide or polynucleotide sequence
CC belonging to the perlecan, precursor of the retinol-binding plasma
CC protein, precursor of the ganglioside GM2 activator, calgranulin B or
CC saposin B protein families. The method is used for detecting,
CC preventing or treating a degenerative, neurological and/or auto-immune
CC disease. The polynucleotides and polypeptides are used for diagnosis,
CC prognosis, prevention and treatment of multiple sclerosis (in its
CC various forms and phases). They may also be useful in cases of
CC e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis,
CC rheumatoid polyarthritis and lupus erythematosus, including use as
CC vaccines and in gene therapy (expression of sense or antisense
CC sequences). They can also be used to assess efficacy of potential
CC therapeutic agents, particularly compounds that reduce or inhibit
CC toxicity towards glial cells.
XX
SQ Sequence 342 BP; 89 A; 31 C; 54 G; 39 T; 129 other;

Query Match

76.0%; Score 262.2; DB 22; Length 342;

Best Local Similarity 62.5%; Pred. No. 2,3e-63;
Matches 213; Conservative 86; Mismatches 42; Indels 0; Gaps 0;

QY 1 atgacttgcacaaatgtcgcagctgcagacgaacatagagacatcatcaacacctcac 60
|||||
DB 1 atgacntgyaartgtgncarytngarmgnaayathgaracnathathaaycnttycay 60
QY 61 caatactctgtgaagctggggacccagacacccctgaaccagggggaattcaagaagctg 120
|||||
DB 61 cartaywsnngtnaarytngncaycngayacnytnaaycargngarttlyaargarytn 120
QY 121 gtgcgaaagatctgcacaaatttctcaagaagagaaataagaatcaaggltcaataga 180
|||||
DB 121 gltmgnaaragayltnaarayltytnaaraaargaraayaaraayargaytnatngar 180
QY 181 cacatcatgagagcctgcagacacaaatgcagacaaagcagctgcagagagttcatc 240
|||||
DB 181 cayathatgagargaytngayacnaaycngayaaarcarytmsntlygargarttyath 240
QY 241 atgctgatgagagagctaaccttgagcctccacagagaagaatgcagaggttgcagaggc 300
|||||
DB 241 atgyltnatgcmngytnacnttgscmwncaygaraaratgcayargngayargagn 300
QY 301 cctggccacacacataagccagagcctcgaggagagggacccc 341
|||||
DB 301 ccngnncaycaycaarccmngytnngngargagnacnc 341

RESULT 11
AAI60936
ID AAI60936 standard; cDNA; 345 BP.
XX
AC AAI60936;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 4925.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KM peripheral nervous system; neuropathy; central nervous system; CNS;
KM Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KM leukaemia; ss.
XX
XX Homo sapiens.
XX
OS
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0522317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HSE-) HXSEQ INC.
XX
XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AU, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX P-PSDB: AAM41780.
XX
DR Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

```
XX XX Claim 1; SEQ ID NO 4925; 10078pp; English.
PS PS
CC CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC CC the encoded polypeptides (AA38642-AA42213) with nucleotide,
CC CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC CC of the invention may be used to treat diseases of the peripheral nervous
CC CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC CC localised neuropathies and central nervous system diseases, such as
CC CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC CC utilisation of the activities such as: Immune system suppression,
CC CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC CC C.N.S disorders.
CC CC Note: The sequence data for this patent did not form part of the printed
CC CC specification.
XX XX
SQ Sequence 345 BP; 110 A; 86 C; 81 G; 68 T; 0 other;

Query Match          75.8%; Score 261.6; DB 22; Length 345;
Best Local Similarity 88.0%; Pred. No. 3.3e-63;
Matches 285; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 atgacttgcaaatgtcgcagctggaacgcacatagagaccatcatcaacaccttcac 60
Db 21 atgacttgcaaatgtcgcagctggaacgcacatagagaccatcatcaacaccttcac 80
QY 61 caatactctgtgaagctcggggcaccgcagacacctgaaccagggggaattcaagaagctg 120
Db 81 catactctgaagagctcggggcaccgcagacacctgaaccagggggaattcaagaagctg 140
QY 121 gtgcgaaaagatctgcgcaaatcttctcaagaagagataagatgaagaagctcagaa 160
Db 141 gtgcgaaacagatctgcgcaaatcttctcaagaagagataagatgaagaagctcagaa 200
QY 181 cacatcatgagagacccctggacacaatgtcagacagaagcattgcgcagagctcattc 240
Db 201 cacatcatgagagacccctggacacaatgtcagacagaagcattgcgcagagctcattc 260
QY 241 atgctgtgtgcgaggtctaactctggtcctccacagagaagatgcagagaggtgcagggc 300
Db 261 atgctgtgtgcgaggtctaactctggtcctccacagagaagatgcagagaggtgcagggc 320
QY 301 cctggcaccaccataaagccagagc 324
Db 321 cctgtgtcaacaacataagccagagc 344

RESULT 12
AAC06727
ID AAC06727 standard; cDNA; 385 BP.
XX
AC AAC06727;
XX
XX 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 10802.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
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```
PR 26-FEB-1999; 99US-0122487.
XX
XX (GEST) GENSET.
XX
XX Dumas Maline Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 10802; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX cDNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX They are used to obtain upstream regulatory sequences and to design
XX expression and secretion vectors.
XX
SQ Sequence 385 BP; 116 A; 104 C; 104 G; 59 T; 2 other;

Query Match          75.4%; Score 260.2; DB 21; Length 385;
Best Local Similarity 89.1%; Pred. No. 8.6e-63;
Matches 304; Conservative 2; Mismatches 0; Indels 35; Gaps 1;

QY 1 atgacttgcaaatgtcgcagctggaacgcacatagagaccatcatcaacaccttcac 60
Db 48 atgacttgcaaatgtcgcagctggaacgcacatagagaccatcatcaacaccttcac 107
QY 61 caatactctgtgaagctcggggcaccgcagacacctgaaccagggggaattcaagaagctg 120
Db 108 catactctgtgaagctcggggcaccgcagacacctgaaccagggggaattcaagaagctg 167
QY 121 gtgcgaaaagatctgcgcaaatcttctcaagaagagataagatgaagaagctcagaa 180
Db 168 gtgcgaaaagatctgcgcaaatcttctcaagaagagataagatgaagaagctcagaa 192
QY 181 cacatcatgagagacccctggacacaatgtcagacagaagcattgcgcagagctcattc 240
Db 193 cacatcatgagagacccctggacacaatgtcagacagaagcattgcgcagagctcattc 252
QY 241 atgctgtgtgcgaggtctaactctggtcctccacagagaagatgcagagaggtgcagggc 300
Db 253 atgctgtgtgcgaggtctaactctggtcctccacagagaagatgcagagaggtgcagggc 312
QY 301 cctggcaccaccataaagccagagcctcggggagggcacc 341
Db 313 cctggcaccaccataaagccagagcctcggggagggcacc 353

RESULT 13
AAF54715/C
ID AAF54715 standard; DNA; 430 BP.
XX
AC AAF54715;
XX
XX 15-MAY-2001 (first entry)
XX
DE Nucleotide sequence of a human polynucleotide sequence.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
```

KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy; ss.
OS Homo sapiens.
XX
XX WO200105422-A2.
XX
XX 25-JAN-2001.
XX
XX 17-JUL-2000; 2000WO-FR02057.
XX
XX 15-JUL-1999; 99FR-0009372.
XX
XX (INMR) BIOMERIEUX STELHYS.
XX
XX Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX
XX WPI; 2001-159475/16.
XX
XX
XX Detecting, preventing and treating degenerative, neurological and
XX autoimmune diseases, particularly multiple sclerosis, using specified
XX polypeptides or related nucleic acid or ligand -
XX
XX
XX Claim 11; Page 186; 209pp; French.
XX
XX
XX The present sequence represents a human polynucleotide sequence, which
XX is used in the method of the invention. The specification describes a
XX method which uses at least one polypeptide or polynucleotide sequence
XX belonging to the perlecan, precursor of the retinol-binding plasma
XX protein, precursor of the ganglioside GM2 activator, calgranulin B or
XX saposin B protein families. The method is used for detecting,
XX preventing or treating a degenerative, neurological and/or auto-immune
XX disease. The polynucleotides and polypeptides are used for diagnosis,
XX prognosis, prevention and treatment of multiple sclerosis (in its
XX various forms and phases). They may also be useful in cases of
XX e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis,
XX rheumatoid polyarthritis and lupus erythematosus, including use as
XX vaccines and in gene therapy (expression of sense or antisense
XX sequences). They can also be used to assess efficacy of potential
XX therapeutic agents, particularly compounds that reduce or inhibit
XX toxicity towards glial cells.
XX
XX
XX Sequence 430 BP; 68 A; 125 C; 120 G; 117 T; 0 other;

Query Match 70.1%; Score 242; DB 22; Length 430;
Best Local Similarity 100.0%; Pred. No. 1e-57;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 104 gggaattcaaaagagctgtgcgaaagaatcgtcaaaatttctcaagaaggaataaga 163
|||
DB 430 GGGAAATTCNAAGAGCTGTGGCAAAAGATCTGCNAATTTTCTCAAGAGAGATAGAG 371
|||
YY 164 atgaaaggtcatagaaacatcatgtgaggaactgtgacacaatgtcagaacagctga 223
|||
DB 370 ATGAAAAGGCTCATTAACACATCATGAGGAGCTGGACACAAATGCGAACAAGCAGCTGA 311
|||
YY 224 gcttcgagagatcatcatctgtatgctgagagctaaacctgtgacctccacagaagaatgc 283
|||
DB 310 GCTTGAAGAGATTCTCATCTGCTGATGGGAGGCTTAACCTGGGCTCCACAGAGAGATTGC 251
|||
YY 284 acgagaggtgacgagggcccttgccaccacccaataagcagagccttcgggagagacccct 343
|||
DB 250 ACGAGGGTGACGAGGGCCCTGGCCACACCATTAAGCAGGCTGGGAGAGGCGACCCCT 191
|||
YY 344 aa 345
|||
DB 190 AA 189

RESULT 14
AAF54713/c

ID AAF54713 standard; DNA; 425 BP.
XX
XX AAF54713;
AC
XX
XX 15-MAY-2001 (first entry)
DT
XX
XX Nucleotide sequence of a human polynucleotide sequence.
DE
XX
XX
XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX WO200105422-A2.
XX
XX 25-JAN-2001.
XX
XX 17-JUL-2000; 2000WO-FR02057.
XX
XX 15-JUL-1999; 99FR-0009372.
XX
XX (INMR) BIOMERIEUX STELHYS.
XX
XX Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX
XX WPI; 2001-159475/16.
XX
XX
XX Detecting, preventing and treating degenerative, neurological and
XX autoimmune diseases, particularly multiple sclerosis, using specified
XX polypeptides or related nucleic acid or ligand -
XX
XX
XX Claim 11; Page 185-186; 209pp; French.
XX
XX
XX The present sequence represents a human polynucleotide sequence, which
XX is used in the method of the invention. The specification describes a
XX method which uses at least one polypeptide or polynucleotide sequence
XX belonging to the perlecan, precursor of the retinol-binding plasma
XX protein, precursor of the ganglioside GM2 activator, calgranulin B or
XX saposin B protein families. The method is used for detecting,
XX preventing or treating a degenerative, neurological and/or auto-immune
XX disease. The polynucleotides and polypeptides are used for diagnosis,
XX prognosis, prevention and treatment of multiple sclerosis (in its
XX various forms and phases). They may also be useful in cases of
XX e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis,
XX rheumatoid polyarthritis and lupus erythematosus, including use as
XX vaccines and in gene therapy (expression of sense or antisense
XX sequences). They can also be used to assess efficacy of potential
XX therapeutic agents, particularly compounds that reduce or inhibit
XX toxicity towards glial cells.
XX
XX
XX Sequence 425 BP; 68 A; 124 C; 117 G; 115 T; 1 other;

Query Match 69.9%; Score 241; DB 22; Length 425;
Best Local Similarity 99.6%; Pred. No. 2e-57;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

YY 104 gggaattcaaaagagctgtgcgaaagaatcgtcaaaatttctcaagaaggaataaga 163
|||
DB 425 GGGAAATTCNAAGAGCTGTGGCAAAAGATCTGCNAATTTTCTCAAGAGAGATAGAG 366
|||
YY 164 atgaaaggtcatagaaacatcatgtgaggaactgtgacacaatgtcagaacagctga 223
|||
DB 365 ATGAAAAGGCTCATTAACACATCATGAGGAGCTGGACACAAATGCGAACAAGCAGCTGA 306
|||
YY 224 gcttcgagagatcatcatctgtatgctgagagctaaacctgtgacctccacagaagaatgc 283
|||
DB 305 GCTTGAAGAGATTCTCATCTGCTGATGGGAGGCTTAACCTGGGCTCCACAGAGAGATTGC 246
|||
YY 284 acgagaggtgacgagggcccttgccaccacccaataagcagagccttcgggagagacccct 343
|||

Db 245 ACGAGGTCGAGGCGCCCTGGCCACCACCATAGCCAGGCGCTGGGAGGACCCCT 186
OY 344 aa 345
11
Db 185 AA 184

RESULT 15
ABA59810/c
ID ABA59810 standard; DNA; 592 BP.

AC ABA59810;

DT 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #8115.

XX Human: foetal liver: gene expression: single exon nucleic acid probe; ss.

XX Homo sapiens.

XX MO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human fetal liver -

XX Claim 1; SEQ ID NO 8115; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for

XX measuring human gene expression in a sample derived from human foetal

XX liver. The single exon nucleic acid probes may be used for predicting,

XX measuring and displaying gene expression in samples derived from human

XX fetal liver. The present sequence is a single exon nucleic acid

XX probe of the invention.

XX Note: The sequence data for this patent did not form part of the

XX printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 592 BP; 111 A; 150 C; 191 G; 140 T; 0 other;

Query Match 57.1%; Score 197; DB 22; Length 592;

Best Local Similarity 100.0%; Pred. No. 4e-45;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 agaaggaataaagatgaagacatagacacatcatgtagagacactgagacacaatg 208

Db 526 AGAAGGAAATTAAGATGAAGGTCATAGAACATCATGAGGACCTGGACACAATG 467

OY 209 cagacaagcagctgagctcgagaggttcacatgctgatgagcagagctaaacctggcct 268

Db 466 CAGACAAGCAGCTGAGCTTCGAGGAGTTTCATCATGCTGATGGGAGGCTAACCTGGGCT 407

OY 269 Tccatgagaagatgacagaggtgacagagggcctgagccacacataagccagagcctcg 328

Db 406 CCCACGAGAAAGATGSCACGAGGAGGTCGAGGAGGCGCCCTGGCCACACCATTAAGCCAGGCTCG 347
OY 329 gggagggcaccocctaa 345
11
Db 346 GGGAGGGCACCCCTTAA 330

Search completed: September 10, 2002, 06:49:30
Job time: 5206 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 06:07:54 ; Search time 2463.79 Seconds
(without alignments)
1889.954 Million cell updates/sec

Title: US-09-806-382a-2
Perfect score: 345
Sequence: 1 atgactgcgaatgacgcga.....tcggggagggcaccacctaa 345

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estmu:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345	100.0	539	10	BE551799 ht86d01.x
2	345	100.0	567	9	AI952029 wx46a07.x
3	345	100.0	582	10	BM008345 603617323
4	345	100.0	609	10	BC438100 602490368
5	345	100.0	638	9	AW964579 EST376652
6	345	100.0	754	10	BC331778 602432209
7	345	100.0	781	10	BE787206 601476885
8	345	100.0	935	10	BI907927 603069064
9	344	99.7	524	9	AA587142 nn70d09.s
10	344	99.7	786	10	BC488718 602534663
11	343.4	99.5	553	10	BE350359 ht75a03.x
12	343.4	99.5	680	10	BI837657 603086883
13	341.8	99.1	561	10	BF511375 UI-H-B14-
14	341	98.8	1190	10	BE785947 601477976
15	333	96.5	500	10	BI518253 603042106
16	333	96.5	573	10	BI760899 603043772
17	333	96.5	576	10	BE786188 601474308

18	333	96.5	725	10	BC332100	BC332100 602432509
19	333	96.5	801	10	BC437703	BC437703 602488965
20	333	96.5	887	10	BC331032	BC331032 602431694
21	333	96.5	907	10	BI836342	BI836342 603083037
22	333	96.5	968	10	BI910664	BI910664 603070429
23	332.2	96.3	399	10	BI031826	BI031826 IL5-MT026
24	329.8	95.6	404	10	BE941564	BE941564 natf04b01.
25	329.2	95.4	404	10	BE784331	BE784331 601473479
26	327.2	94.8	569	9	AW269689	AW269689 xv55d03.x
27	326.6	94.7	423	9	AA587152	AA587152 nn7a10.s
28	323.4	93.6	525	9	AA846123	AA846123 ak83h08.s
29	323.2	93.6	603	10	BC438172	BC438172 602490260
30	321.6	93.2	513	10	BE350415	BE350415 ht85d06.x
31	321	93.0	576	10	BE183248	BE183248 601809954
32	321	93.0	863	10	BE787379	BE787379 601479508
33	321	93.0	1015	10	BI517687	BI517687 603042106
34	320	92.8	557	9	AA586741	AA586741 nn71a07.s
35	316.4	91.7	781	10	BF240407	BF240407 601905958
36	310.4	90.0	548	9	AA583988	AA583988 nn60h02.s
37	307	89.0	547	9	AI281728	AI281728 ct73d01.x
38	303.8	88.1	437	10	W76577	W76577 zd66a09.r1
39	302	87.5	871	10	BE787611	BE787611 601481715
40	301	87.2	891	10	BI839178	BI839178 603085908
41	293	84.9	508	9	AA582879	AA582879 nn72c01.s
42	286.4	83.0	295	10	BE714495	BE714495 PM4-HT072
43	283.6	82.2	540	9	AA586920	AA586920 nn68f07.s
44	281.2	81.5	566	9	AW468067	AW468067 he31e04.x
45	279.4	81.0	307	9	AA320692	AA320692 EST23134

ALIGNMENTS

RESULT 1
BE551799 539 bp mRNA linear EST 10-AUG-2000
LOCUS ht86d01.x1 NCI CGAP HN15 Homo sapiens CDNA clone IMAGE:3159361
DEFINITION similar to gb:X06233 CALGRANULIN B (HUMAN);, mRNA sequence.

ACCESSION BE551799
VERSION BE551799.1 GI:9793491
KEYWORDS EST.
SOURCE human.
ORANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NCI/NIH-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Edward J. Shillitoe, Ph.D., Chlehanok
Leeethanakul, D.D.S.
CDNA Library Preparation: Krizman and Leeethanakul Laboratories
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to: info@image.lnl.gov
Seq primer: -40up from Gibco
High quality sequence stop: 437.

FEATURES

source
1..539
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3159361"
/clone_lib="NCI CGAP HN15"
/tissue_type="Leukoplakia of the buccal mucosa"
/lab_host="DH10B"
/note="Organ: mouth; Vector: pAMP10; mRNA made from leukoplakia, CDNA made by oligo-dT priming.
Non-directionally cloned into UDG sites. Size-selected on

agarose gel, average insert size 500 bp. Primary library.
CDNA Library Preparation: David B. Krizman, Ph.D.
REFERENCE: Krizman et al. (1996) Cancer Research
56:5380-5383 "

BASE COUNT 154 a 159 c 146 g 80 t

ORIGIN

Query Match 100.0%; Score 345; DB 10; Length 539;
Best Local Similarity 100.0%; Pred. No. 5.9e-71;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgacttcgaaatgtgcagctggaagcgaactagaagccatccatcaacaccttcac 60
 |||||||
Db 62 atgacttcgaaatgtgcagctggaagcgaactagaagccatccatcaacaccttcac 121
 |||||||
QY 61 caatactctgtgaagcttggcagccacagacaccccttgaaacagggggaattcaagaagctg 120
 |||||||
Db 122 caatgactctgtgaagcttggcagccacagacaccccttgaaacagggggaattcaagaagctg 181
 |||||||
QY 121 gtgcgaaaaagatctgcgaaattttctcaagaagagaataagatgaaaggtcatagaa 180
 |||||||
Db 182 gtgcgaaaaagatctgcgaaattttctcaagaagagaataagatgaaaggtcatagaa 241
 |||||||
QY 181 ccaatcatggagagacctgtgacacaaatgcagacaagcagctgagcttcgagaggtcatc 240
 |||||||
Db 242 ccaatcatggagagacctgtgacacaaatgcagacaagcagctgagcttcgagaggtcatc 301
 |||||||
QY 241 atgctgatatggagagcttaacctgtgacctccacgagaagatgcagaggtgtgacagagc 300
 |||||||
Db 302 atgctgatatggagagcttaacctgtgacctccacgagaagatgcagaggtgtgacagagc 361
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QY 301 cctggcaccacacataagcagagcctcgaggagggcaaccccttaa 345
 |||||||
Db 362 cctggcaccacacataagcagagcctcgaggagggcaaccccttaa 406

RESULT 2
AI952029 567 bp mRNA linear EST 09-MAR-2000
LOCUS wx46a07.x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2546676 3'
DEFINITION similar to gb:X06233 CALGRANULIN B (HUMAN);, mRNA sequence.
ACCESSION AI952029
VERSION AI952029.1 GI:5744339
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 567)
AUTHORS NCI-CGAP htcp://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbbs-remail.nih.gov
 Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
 Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bdrip/image/image.html
 Insert Length: 413 Std Error: 0.00
 Seq primer: -400P from Gldco
 High quality sequence stop: 408.
 Location/Qualifiers
 1..567
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2546676"
 /clone_lib="NCI_CGAP_Lu28"

FEATURES

source
1..567
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2546676"
/clone_lib="NCI_CGAP_Lu28"

/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."

BASE COUNT 91 a 157 c 159 g 160 t

ORIGIN

Query Match 100.0%; Score 345; DB 9; Length 567;
Best Local Similarity 100.0%; Pred. No. 5.9e-71;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgacttcgaaatgtgcagctggaagcgaactagaagccatccatcaacaccttcac 60
 |||||||
Db 537 atgacttcgaaatgtgcagctggaagcgaactagaagccatccatcaacaccttcac 478
 |||||||
QY 61 caatactctgtgaagcttggcagccacagacaccccttgaaacagggggaattcaagaagctg 120
 |||||||
Db 477 caatgactctgtgaagcttggcagccacagacaccccttgaaacagggggaattcaagaagctg 418
 |||||||
QY 121 gtgcgaaaaagatctgcgaaattttctcaagaagagaataagatgaaaggtcatagaa 180
 |||||||
Db 417 gtgcgaaaaagatctgcgaaattttctcaagaagagaataagatgaaaggtcatagaa 358
 |||||||
QY 181 ccaatcatggagagacctgtgacacaaatgcagacaagcagctgagcttcgagaggtcatc 240
 |||||||
Db 357 ccaatcatggagagacctgtgacacaaatgcagacaagcagctgagcttcgagaggtcatc 298
 |||||||
QY 241 atgctgatatggagagcttaacctgtgacctccacgagaagatgcagaggtgtgacagagc 300
 |||||||
Db 297 atgctgatatggagagcttaacctgtgacctccacgagaagatgcagaggtgtgacagagc 238
 |||||||
QY 301 cctggcaccacacataagcagagcctcgaggagggcaaccccttaa 345
 |||||||
Db 237 cctggcaccacacataagcagagcctcgaggagggcaaccccttaa 193

RESULT 3
BM008345 582 bp mRNA linear EST 30-OCT-2001
LOCUS 603617323P1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450668 5',
DEFINITION mRNA sequence.
ACCESSION BM008345
VERSION BM008345.1 GI:16522699
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS NIH-MGC htcp://mgc.ncbi.nlm.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 htcp://image.llnl.gov
 Plate: LCM1939 row: m column: 05
 High quality sequence stop: 581.
 Location/Qualifiers
 1..582
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5450668"
 /clone_lib="NIH_MGC_113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:

FEATURES

source
1..582
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5450668"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:

ECORI: cDNA made by oligo-dT priming. Directionally cloned into EcorI/XhoI sites using the following 5' adaptor: GGCGAGG(5). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 174 a 159 c 157 g 92 t
ORIGIN

Query Match 100.0%; Score 345; DB 10; Length 582;
Best Local Similarity 100.0%; Pred. No. 6e-71;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgactgtcaaaatgtcgacgtgtgaacgacaatagagaccatcaacaccttcac 60
|||||
DB 32 ATGACTGTGCAAAATGTCTGACGCTGGAACGCAACATAGACCATCATCAACCTTCAC 91
QY 61 caatactctgtgaagctgtgggacccagacacccctgaacccaggggaattcaagagctg 120
|||||
DB 92 CAATACTCTGTGAAGCTGGGGCACCCAGACACCTGTAACCAAGGGGAATTCAAGAGCTG 151
QY 121 gtgcgaaaagatctgcgaaaattttctcaagaagaagaataagaatgaagaagtcatagaa 180
|||||
DB 152 GTGCGAAAGATCTGCAAAATTTTCTCAAGAGAGAAATGAAGATGAAGAGCTCATAGAA 211
QY 181 cacatcatgtgagagctgtgacacaatgtgacagaacgactgtgaatttcgagaagttcatc 240
|||||
DB 212 CACATCATGTGAGAGACCTGGAACAAATGCAACAAAGCACTGCTTCAGAGAGTTTCATC 271
QY 241 atgctgatgtgcagagctgaacccctgggctcccaagagaagaatgcagaaggttacaagagtc 300
|||||
DB 272 ATGCTGATGTGCGAGGCTAATCTGGGGCTCCCAAGAGAAATGACAGAGGTTACGAGCGC 331
QY 301 cctggccacacacataagccagggcctcgaggaggagggacccccctaa 345
|||||
DB 332 CCGTGGCCACACCATTAAGCCAGGCTCGGGGAGGGGACCCCTTA 376

RESULT 4
BG438100 609 bp mRNA linear EST 14-MAR-2001
LOCUS 602490368F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4622272 5',
DEFINITION mRNA sequence.
ACCESSION BG438100
VERSION BG438100.1 GI:13344606
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 609)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DPH/Gazdar
CDNA Library Preparation: Ling Hong/Rubin laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LICM1386 row: h column: 17
High quality sequence stop: 595.
Location/Qualifiers

FEATURES
source 1..609
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4622272"
/clone_1lb="NIH_MGC_18"

BASE COUNT 206 a 160 c 154 g 89 t
ORIGIN

Query Match 100.0%; Score 345; DB 10; Length 609;
Best Local Similarity 100.0%; Pred. No. 6.1e-71;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgactgtcaaaatgtcgacgtgtgaacgacaatagagaccatcaacaccttcac 60
|||||
DB 28 ATGACTGTGCAAAATGTCTGACGCTGGAACGCAACATAGACCATCATCAACCTTCAC 87
QY 61 caatactctgtgaagctgtgggacccagacacccctgaacccaggggaattcaagagctg 120
|||||
DB 88 CAATACTCTGTGAAGCTGGGGCACCCAGACACCTGTAACCAAGGGGAATTCAAGAGCTG 147
QY 121 gtgcgaaaagatctgcgaaaattttctcaagaagaagaataagaatgaagaagttcatagaa 180
|||||
DB 148 GTGCGAAAGATCTGCAAAATTTTCTCAAGAGAGGAATGAAGATGAAGAGCTCATAGAA 207
QY 181 cacatcatgtgagagctgtgacacaatgtgacagaacgactgtgaatttcgagaagttcatc 240
|||||
DB 208 CACATCATGTGAGAGACCTGGAACAAATGCAACAAAGCACTGCTTCAGAGAGTTTCATC 267
QY 241 atgctgatgtgcagagctgaacccctgggctcccaagagaagaatgcagaaggttacaagagtc 300
|||||
DB 268 ATGCTGATGTGCGAGGCTAATCTGGGGCTCCCAAGAGAAATGACAGAGGTTACGAGCGC 327
QY 301 cctggccacacacataagccagggcctcgaggaggagggacccccctaa 345
|||||
DB 328 CCGTGGCCACACCATTAAGCCAGGCTCGGGGAGGGGACCCCTTA 372

RESULT 5
AW964579 638 bp mRNA linear EST 01-JUN-2000
LOCUS AW964579
DEFINITION EST376652 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence.
ACCESSION AW964579
VERSION AW964579.1 GI:8154415
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 638)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@ligr.org
Plate: 203
Seq primer: Reverse.

FEATURES
source 1..638
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 185 a 174 c 167 g 110 t 2 others
ORIGIN

/clone_lib="MAGE_resequences", MACH"
/note="Vector: pbluescriptskm"

Query Match 100.0%; Score 345; DB 9; Length 638;
Best Local Similarity 100.0%; Pred. No. 6.2e-71;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgactctgaaatgctgcagctggaacgaacatagagaccatcatcaacaccttcac 60
|||||
DB 22 ATGACTCTGCAAAATCTCCGACGTGAGACGACATAGACCATCATCAACACCTTCAC 81
OY 61 caatactctgtaagctgagggacccaacacacccctgaaacgaagggaattcaaaagctg 120
|||||
DB 82 CAATACCTGTGAGCTGGGGGACCCAGACACCTGAACGAGGGGAATCAAGAGACTG 141
OY 121 gtgcgaaaaagatctgcaaatcttctcaagaagagaaataagaatgaagatcatagaa 180
|||||
DB 142 GTGCGAAAAGATCTCAAAATTTCTCAAGAAAGAAATGAATGAAGGTCAATGAA 201
OY 181 caatcatagagagacctggaacaaatgacagacagctgagcttcgagagatcatc 240
|||||
DB 202 CACATCATGAGAGACCTGGACACAATGACAGACAGCTGAGCTTCGAGAGATTTCATC 261
OY 241 atgctgtagcgagagcttaacctggtgctccacgagagaatgacagaggtgacagagc 300
|||||
DB 262 ATGCTGATGGCGAGCTTAACCTGGGCTCCACAGAGAAAGATGACGAGGGTGACGAGGGC 321
OY 301 cctggcaccacacataagccagagctcgggagagagacccctaa 345
|||||
DB 322 CCTGGCACACCATTAAGCAGAGCCCTCGGGAGGGCACCCCTTA 366

RESULT 6
BG331778 754 bp mRNA linear EST 27-FEB-2001
LOCUS 602432209F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:454989 5',
DEFINITION
MACH sequence.
ACCESSION BG331778
VERSION BG331778.1 GI:1318216
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 754)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCPD/DTF/Gazdar
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM1242 row: a column: 03
High quality sequence stop: 563.
Location/Qualifiers
1..754

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="454989"
/clone_lib="NIH_MGC_18"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pDRB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:

BASE COUNT 229 a 243 c 189 g 93 t
ORIGIN

Query Match 100.0%; Score 345; DB 10; Length 754;
Best Local Similarity 100.0%; Pred. No. 6.5e-71;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgactctgaaatgctgcagctggaacgaacatagagaccatcatcaacaccttcac 60
|||||
DB 31 ATGACTCTGCAAAATGCTCCGACGTGAGACGACATAGACCATCATCAACACCTTCAC 90
OY 61 caatactctgtaagctgagggacccaacacacccctgaaacgaagggaattcaaaagctg 120
|||||
DB 91 CAATACCTGTGAGCTGGGGGACCCAGACACCTGGAACGAGGGGAATTCAAAGAGCTG 150
OY 121 gtgcgaaaaagatctgcaaatcttctcaagaagagaaataagaatgaagatcatagaa 180
|||||
DB 151 GTGCGAAAAGATCTCAAAATTTCTCAAGAAAGAAATGAATGAAGGTCAATGAA 210
OY 181 caatcatagagagacctggaacaaatgacagacagctgagcttcgagagatcatc 240
|||||
DB 211 CACATCATGAGAGACCTGGACACAATGACAGACAGCTGAGCTTCGAGAGATTTCATC 270
OY 241 atgctgtagcgagagcttaacctggtgctccacgagagaatgacagaggtgacagagc 300
|||||
DB 271 ATGCTGATGGCGAGCTTAACCTGGGCTCCACAGAGAAAGATGACGAGGGTGACGAGGGC 330
OY 301 cctggcaccacacataagccagagctcgggagagagacccctaa 345
|||||
DB 331 CCTGGCACACCATTAAGCAGAGCCCTCGGGAGGGCACCCCTTA 375

RESULT 7
BE787206 781 bp mRNA linear EST 20-OCT-2000
LOCUS 601476885F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:387969 5',
DEFINITION
MACH sequence.
ACCESSION BE787206
VERSION BE787206.1 GI:10208404
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 781)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCPD/DTF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM9645 row: j column: 22
High quality sequence stop: 545.
Location/Qualifiers
1..781

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="387969"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"

/note="Organ: Lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."

BASE COUNT 261 a 214 c 220 g 86 t

Query Match 100.0%; Score 345; DB 10; Length 781;
Best Local Similarity 100.0%; Pred. No. 6.5e-71;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgacttgcgaatgtcgcagctggaagcagacatagaccatcacacacattccac 60
DB 10 ATGACTTGCGAATGTCCAGCTGSAAGCAACATAGAGACATCATCAACACCTTCAC 69
OY 61 caatactctgtgaagctggtgggacccagacacccctgaagcagggaattcaaaagctg 120
DB 70 CAATACTCTGTGAAGCTGGGGACCCAGACACCTGAACCGGGGGAATTCAAAGAGCTG 129
OY 121 gtgcgaaaaagatctgcaaaattttctcaagaagagaataaagaatgaagatcatagaa 180
DB 130 GTGCGAAAAAGATCTGCAAAATTTTCTCAAGAAAGGAAATGAAGATGAAGGATAGAA 189
OY 181 cacatcatggaagagacctgagacacaatgacagaagcagctgagcttcgagaggtcatc 240
DB 190 CACATCATGGAAGAGACCTGAGACACAATGACAGAAGCAGAGCTTCGAGAGATTCATC 249
OY 241 atgctgatggaagcagctgaacctgagcctccacagagaagatgagcaggggtgaggaagggc 300
DB 250 ATGCTGATGGCAGAGCTTAACCTGGGCTCCCAAGGAAAGATGCACAGGGTGACGAGGGC 309
OY 301 cctggccaccaccataagcagagcctcgggaggggacccccctaa 345
DB 310 CCGGCCACACCATTAAGCAGAGCCTCGGGAGGGGACCCCTTAA 354

RESULT 8
BI907927 935 bp mRNA linear EST 16-OCT-2001
LOCUS 603069064P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218046 5',
DEFINITION mRNA sequence.

ACCESSION BI907927
VERSION BI907927.1 GI:16170822
KEYWORDS EST

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS 1 (bases 1 to 935)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM11547 row: p column: 15
High quality sequence stop: 574.
Location/Qualifiers

FEATURES
source 1..935
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5218046"
/clone_lib="NIH_MGC_118"
/csize_type="Leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV

(destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

BASE COUNT 309 a 281 c 248 g 97 t

Query Match 100.0%; Score 345; DB 10; Length 935;
Best Local Similarity 100.0%; Pred. No. 6.9e-71;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgacttgcgaatgtcgcagctggaagcagacatagaccatcacacattccac 60
DB 31 ATGACTTGCGAATGTCCAGCTGSAAGCAACATAGAGACATCATCAACACCTTCAC 90
OY 61 caatactctgtgaagctggtgggacccagacacccctgaagcagggaattcaaaagctg 120
DB 91 CAATACTCTGTGAAGCTGGGGACCCAGACACCTGAACCGGGGGAATTCAAAGAGCTG 150
OY 121 gtgcgaaaaagatctgcaaaattttctcaagaagagaataaagaatgaagatcatagaa 180
DB 151 GTGCGAAAAAGATCTGCAAAATTTTCTCAAGAAAGGAAATGAAGATGAAGGATAGAA 210
OY 181 cacatcatggaagagacctgagacacaatgacagaagcagctgagcttcgagaggtcatc 240
DB 211 CACATCATGGAAGAGACCTGAGACACAATGACAGAAGCAGAGCTTCGAGAGATTCATC 270
OY 241 atgctgatggaagcagctgaacctgagcctccacagagaagatgagcaggggtgaggaagggc 300
DB 271 ATGCTGATGGCAGAGCTTAACCTGGGCTCCCAAGGAAAGATGCACAGGGTGACGAGGGC 330
OY 301 cctggccaccaccataagcagagcctcgggaggggacccccctaa 345
DB 331 CCGGCCACACCATTAAGCAGAGCCTCGGGAGGGGACCCCTTAA 375

RESULT 9
AA587142/c 524 bp mRNA linear EST 26-SEP-1997
LOCUS n70d09.s1 NCI CGAP 1ar1 Homo sapiens cDNA clone IMAGE:1089233 3',
DEFINITION similar to gb:X06233 CALGRANDLIN B (HUMAN);, mRNA sequence.

ACCESSION AA587142
VERSION AA587142.1 GI:2397956
KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 524)
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 650 Std Error: 0.00
Seq primer: ~40m3 fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers

FEATURES
source 1..524

source 1. .786

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov
Seq primer: -40UP from Gldpc
High quality sequence stop: 463.
Location/Qualifiers

FEATURES

SOURCE

1..553
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3158284"
/clone.lib="NCI CGAP HN15"
/tissue_type="Leukoplakia of the buccal mucosa"
/lab_host="DH10B"
/note="Organ: mouth. Vector: pAMP10; mRNA made from leukoplakia, cDNA made by oligo-dt priming. Non-directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 500 bp. Primary library. cDNA library preparation: David B. Krizman, Ph.D. REFERENCE: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 153 a 164 c 149 g 87 t
ORIGIN

Query Match 99.5%; Score 343.4; DB 10; Length 553;
Best Local Similarity 99.7%; Pred. No. 1.4e-70;
Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 atgacttgcgaatgtgcagctggaacgcaacatagagacatcatcaacacctccac 60
|||||
DB 70 ATGACTTGCAAAATGTCCAGCTGGAGACCAATAGACCATATCAACACCTTCCAC 129
|||||
OY 61 caatactctgtgaagctggtgggcaaccgaacacctgaaccagggtgaattcaagaagctg 120
|||||
DB 130 CAATACCTGTGTAAGCTGGGGCACCCAGACACCTCTGAACCAAGGGGAATTCAMAGAGCTG 189
|||||
OY 121 gtgcgaagaagactcgaatatttctcaagaagagagaataagatgaagaagctatagaa 180
|||||
DB 190 GTGCGAAAGACTCGCAAAATTTTCTCAAGAGAGAAATAGAAATGAAGAGTCTATAGAA 249
|||||
OY 181 cacatcatggaagactggaacacaatgcagaacagcagctgagcttcgaggaagttcatc 240
|||||
DB 250 CACATCATGTGAGAGACTGTGACACAATGACAGCAAGCAAGCTGAGCTTGGAGAGATTTCATTC 309
|||||
OY 241 atgtctgattggaagctaaacctgtggcctcccaagagaagatgcagaggtgtgaagagggc 300
|||||
DB 310 ATGCTGATGGCAGAGGCTTAACCTGGGCTCTCCACGAGAAATGCACAGAGGTGACGAGGGC 369
|||||
OY 301 cctggccaccaccataagcagagcctcggtggagagggcaccacctaa 345
|||||
DB 370 CCTGGCCACCACCATAGCCAGGCTCTGGGGAGGGACCCCTTAA 414
|||||

RESULT 12
BI837657 680 bp mRNA linear EST 04-OCT-2001
LOCUS 603086883f1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5225853 5',
DEFINITION mRNA sequence.
ACCESSION BI837657
VERSION BI837657.1 GI:15949207
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 680)
NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Contact: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA library Preparation: Life Technologies, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1568 row: e column: 22
High quality sequence stop: 562.
Location/Qualifiers

FEATURES

SOURCE

1..680
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5225853"
/clone.lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen. Vector: pCMV-SPOK6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dt primed and directionally cloned (pcorv site is destroyed upon cloning). Average insert size 1.5 kb. insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH-MGC Library."

BASE COUNT 209 a 190 c 185 g 96 t
ORIGIN

Query Match 99.5%; Score 343.4; DB 10; Length 680;
Best Local Similarity 99.7%; Pred. No. 1.5e-70;
Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 atgacttgcgaatgtgcagctggaacgcaacatagagacatcatcaacacctccac 60
|||||
DB 29 ATGACTTGCAAAATGTCCAGCTGGAGACCAATAGACCATATCAACACCTTCCAC 88
|||||
OY 61 caatactctgtgaagctggtgggcaaccgaacacctgaaccagggtgaattcaagaagctg 120
|||||
DB 89 CAATACCTGTGTAAGCTGGGGCACCCAGACACCTCTGAACCAAGGGGAATTCAMAGAGCTG 148
|||||
OY 121 gtgcgaagaagactcgaatatttctcaagaagagagaataagatgaagaagctatagaa 180
|||||
DB 149 GTGCGAAAGACTCGCAAAATTTTCTCAAGAGAGAAATAGAAATGAAGAGTCTATAGAA 208
|||||
OY 181 cacatcatggaagactggaacacaatgcagaacagcagctgagcttcgaggaagttcatc 240
|||||
DB 209 CACATCATGTGAGAGACTGTGACACAATGACAGCAAGCAAGCTGAGCTTGGAGAGATTTCATTC 268
|||||
OY 241 atgtctgattggaagctaaacctgtggcctcccaagagaagatgcagaggtgtgaagagggc 300
|||||
DB 269 ATGCTGATGGCAGAGGCTTAACCTGGGCTCTCCACGAGAAATGCACAGAGGTGACGAGGGC 328
|||||
OY 301 cctggccaccaccataagcagagcctcggtggagagggcaccacctaa 345
|||||
DB 329 CCTGGCCACCACCATAGCCAGGCTCTGGGGAGGGACCCCTTAA 373
|||||

RESULT 13
BF511375/c 561 bp mRNA linear EST 06-DEC-2000
LOCUS BF511375
DEFINITION U1-H-B14-aog-e-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone
IMAGE:3084782 3', mRNA sequence.
ACCESSION BF511375
VERSION BF511375.1 GI:11594673
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 561)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward
POLYA-yes.

FEATURES

source

Location/Qualifiers

```

1..561
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3084782"
/clone_1id="NCI-CGAP-Sub8"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pMT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; NCI-CGAP-Sub8 is a subtracted library derived from NCI-CGAP-Sub5. The NCI-CGAP-Sub8 library had 2.5 million recombinants. A single-stranded DNA preparation of NCI-CGAP-Sub5 was used as a tracer in a subtractive hybridization with a driver comprising: a pool of clones from NCI-CGAP-Sub5 (IMAGE clone Ids 2732833-2737415, 3068040-3069191; 25% of the driver population), a pool of clones from NCI-CGAP-Sub4 (IMAGE clone Ids 2723592-2729326; 25% of the driver population), NCI-CGAP-Sub6 (pool Air-AU, IMAGE Ids 2728969-2733190; 25% of the driver population), and NCI-CGAP-Sub7 (IMAGE Ids 3069192-3072228, 3081864-3084550; 25% of the driver population). Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_LIB-NCI-CGAP_Lml9
TAG_TISSUE=Lung
TAG_SEQ=CACACG
150 c 155 g 170 t

```

BASE COUNT

86 a 150 c 155 g 170 t

ORIGIN

Query Match 99.1%; Score 341.8; DB 10; Length 561;
Best Local Similarity 99.4%; Pred. No. 3.3e-70;
Matches 343; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 atgactgtcaaatgttcgcagctggaacgcaacatagagaccatcaaccctccac 60
DB 545 ATGACTGTCAAAATGTGCGAGCTGGAACGCAACATAGAGCATCATCAACACCTTCCAC 486
QY 61 caataactctgtgaagctggggcaccagacacctgaaccagggggaattcaagaagctg 120
DB 485 CAATACTCTGTGAAGCTGGGGCACCCAGACACCTGTGAACGAGGGGAATTCAAAAGAGCTT 426
QY 121 gtgcgaagaatctgcgaatcttctcaagaagaagaataagaataaagaagctacagaa 180
DB 425 GTGCGAAAATATCTGCAAAATTTTCTCAAGAAAGAGAAATAGAAATGAAGGTCTATGAA 366
QY 181 cacatcatggaagacctgacacaaatgacagaacagctgagcttcagagagctcacc 240
DB 365 CACATCATGTGAGAGACCTGACACAATGACAGACAGCTGATCTTCGAGGAGTTCATC 306
QY 241 atgctgatggcagagcttaacctggctccacagagaagaatgacagaggtgaagagc 300
DB 305 ATGCTGATGGCGAGGCTTAACCTTGCGCTCCACAGAGAAATGACAGAGCTGACGAGGGC 246
QY 301 cctggcaaccacataagccagagcctcgaggaggagaccacctaa 345
DB 245 CCGAGCCACACACCATAGCCAGGCTCGGGGAGGAGGCCACCCCTTAA 201

```

RESULT 14
BE785947 1190 bp mRNA linear EST 20-OCT-2000
LOCUS BE785947

DEFINITION 601477976F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880747 5', mRNA sequence.
ACCESSION BE785947
VERSION BE785947.1 GI:10207145
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1190)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DBP/gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LAM9648 row: g column: 20
High quality sequence stop: 521.

FEATURES

source

Location/Qualifiers

```

1..1190
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3880747"
/clone_1id="NIH-MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."
416 a 352 c 274 g 148 t

```

BASE COUNT

416 a 352 c 274 g 148 t

ORIGIN

Query Match 98.8%; Score 341; DB 10; Length 1190;
Best Local Similarity 100.0%; Pred. No. 6.5e-70;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 ctgtgcaaatgttcgcagctggaacgcaacatagagaccatcaaccctccacaa 64
DB 1 CTGCAAAATGTGCGAGCTGGAACGCAACATAGAGCATCATCAACACCTTCCACCAT 60
QY 65 actctgtgaagctggggcaccagacacctgaaccagggggaattcaagaagctgtgc 124
DB 61 ACTCTGTGAAGCTGGGGCACCCAGACACCTGTGAACGAGGGGAATTCAAAAGAGCTGTGC 120
QY 125 gaaagaatctgcaaatcttctcaagaagaagaataagaatgaagaagctacagaca 184
DB 121 GAAAAGATCTGCAAAATTTTCTCAAGAAAGAGAAATGAAGAAAGCTCATACACACA 180
QY 185 tcatggaagacctgacacaaatgacagaacagcagctgagcttcagagaagctacatgc 244
DB 181 TCATGAGAGACTGACACAAATGACAGCAAGCACTGACCTTGAGAGAGTTCATATGC 240
QY 245 tgatggcagagctaaacctggcctccacgagaagatgacagaaggtgacagagagcctg 304
DB 241 TGATGGCGAGGCTTAACCTTGCGCTCCACAGAGAAATGACAGAGGTGACGAGGGCCCTG 300
QY 305 gccaccacataagccagagcctcgaggaggagaccacctaa 345
DB 301 GCCACACCATTAAGCCAGGCTCGGGGAGGAGGCCACCCCTTAA 341

```

RESULT 15
B518253 500 bp mRNA linear EST 29-AUG-2001
LOCUS B518253/c
DEFINITION 603042106T1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182609 3',

mRNA sequence.

ACCESSION B1518253
 VERSION B1518253.1 GI:15343045

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 500)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgabds@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LENL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LENL at:

<http://image.llnl.gov>

Plate: L1AM11455 row: 1 column: 02

High quality sequence start: 4

High quality sequence stop: 500.

FEATURES

Source

1..500

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5182609"

/clone_lib="NIH_MGC_116"

/lab_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector:

PCWV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo

female, 71 yo male colon; 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

023. Note: this is a NIH MGC Library."

BASE COUNT

75 a 137 c 141 g 147 t

ORIGIN

Query Match

Best Local Similarity 96.5%; Score 333; DB 10; Length 500;

Matches 344; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Matches 344; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 atgaactgcacaaatgtcgcagctggaacgcacacatagagaccatcatcaacacctccac 60
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DB 470 atgacctgtgcaaaatgtcgcagctggaacgcacacatagagaccatcatcaacacctccac 411
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QY 61 caatctctgtgaagctggggcaccacgaacccctgaaccagggggaattcaagaagctg 120
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DB 410 caatctctgtgaagctggggcaccacgaacccctgaaccagggggaattcaagaagctg 351
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QY 121 gtgcgaaaagatctgcaaatcttctcaagaagagaaataagaatgaagaagtcataagaa 180
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DB 350 gtgcgaaaagatctgcaaatcttctcaagaagagaaataagaatgaagaagtcataagaa 291
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QY 181 caacatcatggaagacctgacacaaatgcagaacagcctgaagcttcgaggagttcatc 240
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DB 290 caacatcatggaagacctgacacaaatgcagaacagcctgaagcttcgaggagttcatc 231
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QY 241 atgcctgatggcagagctaacctgggctccacgagaagatgacagaggtgacgaagc 300
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DB 230 atgcctgatggcagagctaacctgggctccacgagaagatgacagaggtgacgaagc 170
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QY 301 cctggcaccacacataagcgaagcctcgggagggcaccacctaa 345
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DB 171 cctggcaccacacataagcgaagcctcgggagggcaccacctaa 127
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Search completed: September 10, 2002, 06:08:02
 Job time: 6638 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 06:42:40 ; Search time 2062.36 Seconds
(Without alignments)
3500.676 Million cell updates/sec

Title: US-09-806-382a-2
345
Perfect score: 1 atgcactgcgaatgcgca.....tcggggagggcacccctaa 345
Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: GenBank.*
2: gb_ba.*
3: gb_hc.*
4: gb_in.*
5: gb_lm.*
6: gb_ov.*
7: gb_pat.*
8: gb_ph.*
9: gb_pl.*
10: gb_pr.*
11: gb_ro.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
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17: em_hum.*
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20: em_om.*
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31: em_htg_inv.*
32: em_htg_other.*
33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	345	100.0	345	6	AX038706	AX038706 Sequence
2	345	100.0	462	6	AI12029	AI12029 Macrophage
3	345	100.0	462	6	HSMRP14	X06293 Human mRNA
4	345	100.0	565	6	AX332248	AX332248 Sequence
5	345	100.0	565	6	AX333056	AX333056 Sequence
6	345	100.0	565	9	HUMCPA	M26311 Human cysti
7	345	100.0	567	9	HUM2D66A09	AF086362 Homo sapi
8	345	100.0	571	6	AR015928	AF015928 Sequence
9	345	100.0	687	6	AX017310	AX017310 Sequence
10	345	100.0	688	6	AX017255	AX017255 Sequence
11	333	96.5	336	6	AI12024	AI12024 Macrophage
12	187	57.1	1754	6	AI12032	AI12032 PARTIAL Mac
13	197	57.1	4439	6	HUMMRP14A	M21064 Human migra
14	197	57.1	4440	6	I38533	I38533 Sequence 4
15	197	57.1	4804	9	AF237581	AF237581 Homo sapi
16	197	57.1	4804	9	AF237582	AF237582 Homo sapi
17	197	57.1	114364	9	AC011666	AC011666 Human Chr
18	197	57.1	164144	9	AL591704	AL591704 Human DNA
19	197	57.1	278361	2	AL606502	AL606502 Homo sapi
20	165.8	48.1	494	10	RATMRP14	LI8948 Rattus norv
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22	162.4	47.1	480	4	AF091849	AF091849 Oryctolag
23	150	43.5	2737	6	AI12031	AI12031 PARTIAL Mac
24	98.8	28.6	273	6	AR102853	AR102853 Sequence
25	93.2	27.0	429	4	D49548	D49548 Bos taurus
26	93.2	27.0	429	6	AR083233	AR083233 Sequence
27	93.2	27.0	429	6	AR177852	AR177852 Sequence
28	93.2	27.0	429	23	E12013	E12013 cDNA encodi
29	93.2	27.0	429	23	E12020	E12020 cDNA encodi
30	92	26.7	598	5	GG126MRP	X61200 G.gallus 12
31	89.4	25.9	405	4	AF011757	AF011757 Bos tauru
32	88.8	25.7	6991	10	MM0250496	AF011757 Bos tauru
33	84	24.3	167014	2	AC097705	AJ250496 Mus muscu
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36	81.8	23.7	439	9	HSS100PCB	AX330549 Sequence
37	81.8	23.7	516	9	BC006819	X65614 H.sapiens m
38	80.4	23.3	325	6	AX284667	BC006819 Homo sapi
39	80.4	23.3	602	6	AX285010	AX284667 Sequence
40	79	22.9	292	6	AX341277	AX285010 Sequence
41	78.8	22.8	114	4	RABMRP14	AX341277 Sequence
42	78.6	22.8	288	6	AX038716	D17404 Rabbit mRNA
43	78.6	22.8	288	6	AX038718	AX038716 Sequence
44	78.4	22.7	289	6	AX351438	AX038718 Sequence
45	77.4	22.4	441	6	AR083238	AX351438 Sequence

ALIGNMENTS

RESULT 1	AX038706	345 bp	DNA	linear	PAT 16-NOV-2000
LOCUS	AX038706	Sequence 17 from Patent WO0061742.			
DEFINITION	AX038706				
ACCESSION	AX038706				
VERSION	AX038706.1	GI:11228054			
KEYWORDS					
SOURCE					
ORGANISM	human.				
REFERENCE	Human sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.				
JOURNAL	Katus/H.A. and Remppis, A.				
FEATURES	1 (bases 1 to 345)				
SOURCE	Treatment of cardiac power failure				
	Patent: WO 0061742-A 17 19-OCT-2000;				
	KATUS HUGO A (DE) ; REMPPIS ANDREW (DE)				
	Location/Qualifiers				
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BASE COUNT 110 a 89 c 92 g 54 t
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Best Local Similarity 100.0%; Pred. NO.1.2e-73;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 caatactctgtgaagctggtggcaccagacaacctgaaacagggggaattcaagaagctg 120
Db 61 CAATACTCTGTGAAGCTGGGGCCACCCAGACACCTGAACCAAGGGAATTCAAGAGCTG 120
QY 121 gtgcgaaagaatctgcgaatcttctcaagaaggagaataagaatgaagaagtcataagaa 180
Db 121 GTGCGAAAGAATCTGCAAAATTTCTCAGAGAGAGATGAATGAAGCTCATGAA 180
QY 181 cacatcatgagagacctggaacacaatgcaagaagcagctgagcttcgaaggatcattc 240
Db 181 CACATCATGAGAGACCTGGACACAATGCAACAAGCAGCTTCGAGAGATTTCATC 240
QY 241 atgtctgtagcgaagctgaacctggcctcccaagagaagatgcaagaggtgacgaagc 300
Db 241 ATGCTGATGGCGAGGAGCTTAACCTGGGCTCCACGAGAAAGTGCAGAGGTGAGAGGCG 300
QY 301 cctggccaccacataagcagcctcgaggaggccacccctaa 345
Db 301 CCTGGCCACCACTAAGCCAGGCTCGGGGAGGACCCCTTA 345

RESULT 2
LOCUS A12029 462 bp DNA linear PAT 11-JAN-1994
DEFINITION Macrophage migration inhibition factor (MRP-14) from mRNA of a
human mononuclear leukocyte (formula 6).
ACCESSION A12029
VERSION A12029.1 GI:490103
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 462)
Odink,K.G., Clerc,R., Cerletti,N., Brueggel,J., Tarsay,L., Sorg,C.
and Wiesendanger,W.
TITLE Novel lymphokine related peptides
JOURNAL Patent: EP 0263072-A 14 06-APR-1988;
CIBA-GEIGY AG
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
45..389
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/protein_id="CAA01002.1"
/db_xref="GI:490104"
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LONFLKKNKNEKVIIEHIMEDLDITNADKQLSFEFFILMARLTWASHEKMHGDEGPG
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BASE COUNT 139 a 128 c 124 g 71 t
ORIGIN

Query Match 100.0%; Score 345; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. NO.1.2e-73;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgacttgcaaaatgctgcagctggaagcaacatagaccatcatcaaccttcac 60
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QY 61 caatactctgtgaagctggtggcaccagacaacctgaaacagggggaattcaagaagctg 120
Db 105 CAATACTCTGTGAAGCTGGGGCCACCCAGACACCTGAACCAAGGGAATTCAAGAGCTG 164
QY 121 gtgcgaaagaatctgcgaatcttctcaagaaggagaataagaatgaagaagtcataagaa 180
Db 165 GTGCGAAAGAATCTGCAAAATTTCTCAGAGAGAGATGAATGAAGCTCATGAA 224
QY 181 cacatcatgagagacctggaacacaatgcaagaagcagctgagcttcgaaggatcattc 240
Db 225 CACATCATGAGAGACCTGGACACAATGCAACAAGCAGCTTCGAGAGATTTCATC 284
QY 241 atgtctgtagcgaagctgaacctggcctcccaagagaagatgcaagaggtgacgaagc 300
Db 285 ATGCTGATGGCGAGGAGCTTAACCTGGGCTCCACGAGAAAGTGCAGAGGTGAGAGGCG 344
QY 301 cctggccaccacataagcagcctcgaggaggccacccctaa 345
Db 345 CCTGGCCACCACTAAGCCAGGCTCGGGGAGGACCCCTTA 389

RESULT 3
LOCUS HSMRP14 462 bp mRNA linear PRI 12-SEP-1993
DEFINITION Human mRNA for calcium-binding protein in macrophages (MRP-14)
macrophage migration inhibitory factor (MIF)-related protein.
ACCESSION X06233 Y00286
VERSION X06233.1 GI:34770
KEYWORDS calcium binding protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 462)
Odink, K.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1987) Odink K., Ciba-Geigy, Dept. of
Biotechnology, K 681-442, 4002 Basel, Switzerland
2 (bases 1 to 462)
Odink, K., Cerletti, N., Brueggel, J., Clerc, R. G., Tarsay, L.,
Zwadlo, G., Gerhards, G., Schlegel, R., and Sorg, C.
TITLE Two calcium-binding proteins in infiltrate macrophages of
rheumatoid arthritis
JOURNAL Nature 330 (6143), 80-82 (1987)
MEDLINE 88039099
COMMENT MRP-14 is expressed myeloid specific in acute and chronic
inflammation; it is increased in serum of cyclic fibrosis patients
and heterozygotes for this disease
see X06234.
FEATURES
source Location/Qualifiers
1..462
/organism="Homo sapiens"
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45..389
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/db_xref="SWISS-PROT:P06702"
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LONFLKKNKNEKVIIEHIMEDLDITNADKQLSFEFFILMARLTWASHEKMHGDEGPG
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BASE COUNT 139 a 128 c 124 g 71 t
ORIGIN

Query Match 100.0%; Score 345; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.2e-73;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgacttcgaaatgtcgagctgtgaaagcacaatagagaccatcatcaaaccttcac 60
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DB 45 ATGACTTGGAAAATGTCCAGCTGGAGACGAACATAGAGACCATCATCAACCTTCAC 104
|||||
OY 61 caatactctgtgaagctgggagccacagacaacctgaaccaggggaaattcaagagctg 120
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DB 105 CAATTAATCTGTGAAGCTGGGGCACCAGACACCCCTGAACCGAGGGGAATTCAAAAGAGCTG 164
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OY 121 gtgcgaaaagatctgcaaaatttctcaagaagagaatgaatgaagaagttcatgaa 180
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DB 165 GTGCGAAAAGATCTGCAAAATTTTCTCAAGAGAGAAATGAATAAGGTCTATAGAA 224
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OY 181 cacatcatggaagacctgtgacacaatgtgagacaagcgtgagcttcgaagagttcatc 240
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DB 225 CACATCATGAGAGACCTGGACCAAAATGCAAGACAGACTTCAGAGAGTTTCATC 284
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OY 241 atgctgatgagagcttaacctgtggcctcccaagagaatgtcacgaggtgacgagggc 300
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DB 285 ATGCTGATGGCGAGGCTAAGCTGGGCTCCCAAGAAAGATGCAGAGGGTGACGAGGCG 344
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OY 301 cctggccacacacataagccaggcctcgggaggggacccctaa 345
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DB 345 CCGGCCACCCACCATTAAGCCAGGCTCGGGGAGGAGGCCACCCCTTAA 389
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RESULT 4
AX332248
LOCUS AX332248 565 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 2757 from Patent WO0194629.
ACCESSION AX332248
VERSION AX332248.1 GI:18122882
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (sites)
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrihan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 2757 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source 1..565
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 158 a 158 c 156 g 93 t
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Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 92 CAATTAATCTGTGAAGCTGGGGCACCAGACACCCCTGAACCGAGGGGAATTTCAAGAGCTG 151
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OY 121 gtgcgaaaagatctgcaaaatttctcaagaagagaatgaatgaagaagttcatgaa 180
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DB 152 GTGCGAAAAGATCTGCAAAATTTTCTCAAGAGAGACAAATAGATCAAAAGGTCATAGAA 211
OY 181 cacatcatggaagacctgtgacacaatgtcagacaagcagctgagcttcgaagagttcatc 240
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DB 212 CACATCATGAGAGACCTGGAGACCAAAATGCAAGACAGACGTGAGTTTCATC 271
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OY 241 atgctgatgagagcttaacctgtggcctcccaagagaatgtcacgaggtgacgagggc 300
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DB 272 ATGCTGATGGCGAGGCTAAGCTGGGCTCCCAAGAGAGATGACGAGGTCGAGAGGCG 331
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OY 301 cctggccacacacataagccaggcctcgggaggggacccctaa 345
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DB 332 CCGGCCACCCACCATTAAGCCAGGCTGGGGAGGAGGCCACCCCTTAA 376
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RESULT 5
AX333056
LOCUS AX333056 565 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 3565 from Patent WO0194629.
ACCESSION AX333056
VERSION AX333056.1 GI:18123690
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (sites)
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrihan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3565 13-DEC-2001;
Avalon Pharmaceuticals (US)
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source 1..565
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e-73;
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DB 32 ATGACTTGGAAAATGTCCAGCTGGAGACGAACATAGAGACCATCAACACCTTCAC 91
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OY 61 caatactctgtgaagctgggagccacagacaacctgaaccaggggaaattcaagagctg 120
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DB 92 CAATTAATCTGTGAAGCTGGGGCACCAGACACCCCTGAACCGAGGGGAATTTCAAGAGCTG 151
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DB 152 GTGCGAAAAGATCTGCAAAATTTTCTCAAGAGAGAAATGAATAAGGTCTATAGAA 211
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OY 181 cacatcatggaagacctgtgacacaatgtcagacaagcgtgagcttcgaagagttcatc 240
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DB 212 CACATCATGAGAGACCTGGACCAAAATGCAAGACAGACTTCAGAGAGTTTCATC 271
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OY 241 atgctgatgagagcttaacctgtggcctcccaagagaatgtcacgaggtgacgagggc 300
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DB 272 ATGCTGATGGCGAGGCTAAGCTGGGCTCCCAAGAGAGATGACGAGGTCGAGAGGCG 331
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OY 301 cctggccacacacataagccaggcctcgggaggggacccctaa 345
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DB 332 CCGGCCACCCACCATTAAGCCAGGCTCGGGGAGGAGGCCACCCCTTAA 376
|||||

RESULT 6
HUMCFA HUMCFA 565 bp mRNA linear PRI 19-JUN-1995
LOCUS

```

DEFINITION Human cystic fibrosis antigen mRNA, complete cds.
ACCESSION M26311
VERSION M26311.1 GI:862619
KEYWORDS cystic fibrosis antigen; protein kinase inhibitor.
SOURCE Homo sapiens spleen cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 565)
AUTHORS Murao,S., Collart,F.R. and Huberman,E.
TITLE A protein containing the cystic fibrosis antigen is an inhibitor of
JOURNAL protein kinases
MEDLINE J. Biol. Chem. 264 (14), 8356-8360 (1989)
89255276
COMMENT On Jun 19, 1995 this sequence version replaced gi:341463.
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BASE COUNT 158 a 158 c 156 g 93 t
ORIGIN
Query Match 100.0%; Score 345; DB 9; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.2e-73;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 atgacttgcacaaatgtcgcagcttggaagcagaatagaccatcatcaacaccttcac 60
Db ATGACTTGCACAAATGTCGACAGCTGGAAGCAACATAGACATCATCAACACCTTCCAC 91
OY 61 caatcctctgtgaagcttgaggcaccagacacacctgaacacaggagggaatcaagaagctg 120
Db CAATCCTCTGTGAAGCTTGAGGACCCAGACACCTGTGACACAGGGGAAATTCAGAGAGCTG 151
OY 92 caatcctctgtgaagcttgaggcaccagacacacctgaacacaggagggaatcaagaagctg 151
Db CAATCCTCTGTGAAGCTTGAGGACCCAGACACCTGTGACACAGGGGAAATTCAGAGAGCTG 151
OY 121 gtgcgaaagaatctgcacaaatcttctcaagaagagagataagaatgaagaagtcatalaga 180
Db GTGCGAAAGAATCTGCACAAATTTCTCAAGAAGGAGAAATGAAGATGAAGGTCATAGAA 211
OY 181 caatcctctgtgaagcttgaggcaccagacacacctgaacacaggagggaatcaagaagctg 240
Db CAATCCTCTGTGAAGCTTGAGGACCCAGACACCTGTGACACAGGGGAAATTCAGAGAGCTG 271
OY 212 caatcctctgtgaagcttgaggcaccagacacacctgaacacaggagggaatcaagaagctg 271
Db CAATCCTCTGTGAAGCTTGAGGACCCAGACACCTGTGACACAGGGGAAATTCAGAGAGCTG 271
OY 241 atgctgatgtgcagagctaaccttggcctcccaagagaagaatgaacagaggttgacgaagc 300
Db ATGCTGATGTGCAAGAGCTTAACCTGGGCTCCACAGAAATGACAGAGGAGGTGACGAGGCG 331
OY 301 cctgagccacacccaataagccagagcttgaggaggagagagagagagagagagagagagag 345
Db 332 CCTGAGCCACACCCAATAAGCCAGAGCTTGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 376
RESULT 7
LOCUS HUMZD66A09 567 bp mRNA linear PRI 29-AUG-1998
DEFINITION Homo sapiens full length insert cDNA clone ZD66A09.
ACCESSION AF086362
AF086362.1 GI:3483707
VERSION F11.CDNA.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 567)

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AUTHORS Moessner,J., Tan,F., Marra,M., Kucaba,T., Vandell,M., Martin,J.,
Marth,G., Bowles,L., Mylle,T., Bowers,Y., Steptoe,M., Theising,B.,
Geisels,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
Gibbons,M., Harvey,N., Page,D., Chamberlain,A., Morales,R.,
Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L.,
Wilson,R. and Waterston,R.
TITLE Full Clone Sequencing of the longest Available Member from Each
JOURNAL Unigene Cluster
REFERENCE 2 (bases 1 to 567)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
NOTICE: This sequence represents the full insert of this cDNA. No
attempt has been made to verify whether this corresponds to the
full-length of the original mRNA from which it was derived. We
have tried to obtain double-stranded, or double chemistry sequence
across the entire clone, but potentially, there are areas in the
sequence where this level of coverage was not achieved.
Nevertheless, we are confident of the accuracy of this sequence as
all regions of low quality, as defined by PHRAP (P. Green, in
preparation), were visually inspected and edited accordingly. The
consensus quality values for this sequence have been submitted
separately.
SIMILARITY INFORMATION:
Probable match to Homo sapiens protein P06702 (PID:g115444)
CALGRAMULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)
(MRP-14) (P14) (LEUKOCYTE LI COMPLEX HEAVY CHAIN) (S100
CALCIUM-BINDING PROTEIN A9)
The location of this clone is unknown.
FEATURES
source
location/Qualifiers
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/db_xref="taxon:9606"
/clone_image="345592"
/clone_lib="Soares_fetal_heart_NbHH19W"
25..366
/note="probable match to Homo sapiens protein P06702
(PID:g115444)"
37..384
/note="similar to Bos taurus protein A42628
(PID:g1072439)"
37..384
/note="similar to Bos taurus protein P28783 (PID:g399172)"
40..357
/note="similar to Mus musculus protein P31725
(PID:g399173)"
40..360
/note="similar to Rattus norvegicus protein P50116
(PID:g1710814)"
BASE COUNT 166 a 157 c 154 g 90 t
ORIGIN
Query Match 100.0%; Score 345; DB 9; Length 567;
Best Local Similarity 100.0%; Pred. No. 1.2e-73;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 atgacttgcacaaatgtcgcagcttggaagcagaatagaccatcatcaacaccttcac 60
Db 25 ATGACTTGCACAAATGTCGACAGCTGGAAGCAACATAGACATCATCAACACCTTCCAC 84

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QY 61 caatctctgtggaagctggggcaccgagacacccctgtaaccagggggaattcaaaagctg 120
Db 85 CAATACCTCTGTGAAGCTGGGGCACCCAGACACCTGAAACAGGGGGAATTCAAAGACCTG 144
QY 121 gtgcgaaagaatctgcgaatttctcaagaagaataagaatgaagaaggtcatagaa 180
Db 145 GTGGGAAAGATCTGCAAAATTTTCTCAGAGAGAGAAATGAATGAAGAGTATATGAA 204
QY 181 cacatcatgagagacctgagacacaatgacagaagcagctgagcttcgagaggttcac 240
Db 205 CACATCATGAGAGACCTGAGACAAATGACAGACAAGCAGCTGACCTTCGAGAGATTCATC 264
QY 241 atgtctgtagggagagctgaactggtgctcccaagaagaatgcaagggtgtagaagggc 300
Db 265 ATGTCTGATGGGAGAGCTTAACCTGGGCTCCACAGAAAGATGACAGAGGTGACGAGGGC 324
QY 301 cctggccaccacataagccagcctcgaggaggagggaccacctaa 345
Db 325 CCTGGCCACACCATTAAGCCAGGCTCGGGAGGAGGACCCCTTAA 369

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RESULT 8
AR015928
LOCUS AR015928 571 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 4 from patent US 5776348.
ACCESSION AR015928
VERSION AR015928.1 GI:3972205
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 571)
AUTHORS Selengut,J.D., Orme-Johnson,W.H., Drexler,S.P. and Asakura,H.
TITLE Mineral precipitation system and method for inhibiting mineral
JOURNAL precipitate formation
FEATURES Patent: US 5776348-A 07-JUL-1998;
LOCATION/Qualifiers
SOURCE 1..571
BASE COUNT 160 a 160 c 157 g 94 t
ORIGIN

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Query Match 100.0%; Score 345; DB 6; Length 571;
Best Local Similarity 100.0%; Pred. No. 1.2e-73;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 atgacttcaaaatgtgcagctggaacgaacataagaccatcatcaaccttcac 60
Db 44 ATGACTTCAAAATGTGCGACGTGGAACGCAACATAGACCATCATCAACCTTCCAC 103
QY 61 caatctctgtaagctgggacacacacccctgaaccagggggaattcaaaagctg 120
Db 104 CAATACCTCTGTGAAGCTGGGGCACCCAGACACCTGAAACAGGGGAATTAAGACGTG 163
QY 121 gtgcgaaagaatctgcgaatttctcaagaagaataagaatgaagaaggtcatagaa 180
Db 164 GTGGGAAAGATCTGCAAAATTTTCTCAGAGAGAGAAATGAATGAAGAGTATATGAA 223
QY 181 cacatcatgagagacctgagacacaatgacagaagcagctgagcttcgagaggttcac 240
Db 224 CACATCATGAGAGACCTGAGACAAATGACAGACAAGCAGCTGACCTTCGAGAGATTCATC 283
QY 241 atgtctgtagggagagctgaactggtgctcccaagaagaatgcaagggtgtagaagggc 300
Db 284 ATGTCTGATGGGAGAGCTTAACCTGGGCTCCACAGAAAGATGACAGAGGTGACGAGGGC 343
QY 301 cctggccaccacataagccagcctcgaggaggaggaccacctaa 345
Db 344 CCTGGCCACACCATTAAGCCAGGCTCGGGAGGAGGACCCCTTAA 388

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RESULT 9

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AX017310
LOCUS AX017310 687 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 66 from Patent WO947669.
ACCESSION AX017310
VERSION AX017310.1 GI:10042228
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 687)
Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pilarczyk,C.
TITLE Human nucleic acid sequences from tissue of breast tumors
JOURNAL Patent: WO 947669-A 66 23-SEP-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METZGEN GRS FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
FEATURES Location/Qualifiers
SOURCE 1..687
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 177 a 198 c 190 g 122 t
ORIGIN

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Query Match 100.0%; Score 345; DB 6; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.2e-73;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 atgacttgcgaatgtgcagctggaacgaacataagaccatcatcaaccttcac 60
Db 101 ATGACTTGCGAATGTGCGACGTGGAACGCAACATAGACCATCATCAACCTTCCAC 160
QY 61 caatctctgtaagctgggacacacacccctgaaccagggggaattcaaaagctg 120
Db 161 CAATACCTCTGTGAAGCTGGGGCACCCAGACACCTTAAACAGGGGAATTCAAAGAGCTG 220
QY 121 gtgcgaaagaatctgcgaatttctcaagaagaataagaatgaagaaggtcatagaa 180
Db 221 GTGGGAAAGATCTGCAAAATTTTCTCAGAGAGAGAAATGAATGAAGAGTATATGAA 280
QY 181 cacatcatgagagacctgagacacaatgacagaagcagctgagcttcgagaggttcac 240
Db 281 CACATCATGAGAGACCTGAGACAAATGACAGAACACAGCTGAGCTTGAAGAGTTCATC 340
QY 241 atgtctgtagggagagctgaactggtgctcccaagaagaatgcaagggtgtagaagggc 300
Db 341 ATGTCTGATGGGAGAGCTTAACCTGGGCTCCACAGAAAGATGACAGAGGTGACGAGGGC 400
QY 301 cctggccaccacataagccagcctcgaggaggaggaccacctaa 345
Db 401 CCTGGCCACACCATTAAGCCAGGCTCGGGAGGAGGACCCCTTAA 445

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RESULT 10
AX017255
LOCUS AX017255 688 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from Patent WO947669.
ACCESSION AX017255
VERSION AX017255.1 GI:10042173
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 688)
Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pilarczyk,C.
TITLE Human nucleic acid sequences from tissue of breast tumors
JOURNAL Patent: WO 947669-A 5 23-SEP-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METZGEN GRS FUER GENOMFORSCHUN

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(DE); PILARSKY CHRISTIAN (DE)
FEATURES
source 1..688
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 178 a 198 c 190 g 122 t
ORIGIN

Query Match 100.0%; Score 345; DB 6; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.2e-73;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgacctcaaatgctgcagctggaacgacaatagaccatcatcaaaccttcac 60
DB 101 ATGACTTCAAAATGTCGACACTGGAACGCAACATAGACCATATATACCTTTCCAC 160

QY 61 caatctctgtgaagctggtggcaccagacacccctgaaccagggtgaattcaaaagctg 120
DB 161 CAATCTCTGTGAAGCTGGGCGACCCAGACACCCCTGAACACAGGGGAATTCAAAGAGCTG 220

QY 121 gtggcaaaagatctgcgaatttctcagaagaggaataagaataaaggtctagaa 180
DB 221 GTGGCAAAAGATCTGCAAAATTTTCTCAAGAAAGGAATTAAGAAAGGTCTATAGAA 280

QY 181 cacatcatggaagactggaacacaatgacaagaacagcagctgagcttcgagaagttcatc 240
DB 281 CACATCATGGAAGACTGGACACAAATGCAGACAGCAGCTTGAGAGAGTTTCATC 340

QY 241 atgctgtagggagagctaaactggtggtccccaagagaagatgcagaggtgtaacgaagggc 300
DB 341 ATGCTGAGGGGAGGAGCTTAACCTGGGCCCTCCACGAGAAAGATGACAGAGGTGACGAGGGC 400

QY 301 cctggccaccaccataagccagagcctcggtggaggagaccacctaa 345
DB 401 CCTGGCCACACCATAGCCAGGCTCGGGAGGAGGCCCTTA 445

RESULT 11
A12024 336 bp DNA linear PAT 11-JAN-1994
LOCUS
DEFINITION Macrophage migration inhibition factor (MRP-14).
ACCESSION A12024
VERSION A12024.1 GI:491245
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 336)
AUTHORS Odink,K.G., Clerc,R., Cerletti,N., Brueggen,J., Tarcsay,L., Sorg,C.
and Wiesendanger,W.
TITLE Novel lymphokine related peptides
JOURNAL Patent: EP 0263072-A 9 06-APR-1988;
CIBA-GEIGY AG

FEATURES
source 1..336
/organism="synthetic construct"
/db_xref="taxon:32630"
misc_difference 1
/note="n= a flanking DNA residue of 12 nucleotides or more
containing a promoter sequence"
misc_difference 2
/note="n= M,T,C,K or is absent"
gene 3..335
/gene="MRP-14"
CDS 3..335
/gene="MRP-14"
/codon_start=1
/transl_table=11
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/db_xref="GI:491246"
/translation="MSQLEKNITITINTPHQISVYKLGHPDTLNOGKERKEIVKDLQNF
LKKNKNEKVIHEIMEDLDTNADKQLSFEETIMLARLTWASHEKMGDEGPGHHHK

PGIGEGTP"
misc_difference 336
/note="n= a flanking DNA residue of one or more
nucleotides or is absent"
BASE COUNT 105 a 87 c 90 g 51 t 3 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1e-70;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 atgtgcagctggaacggaacatagagaccatcatcaaaccttcacaaactctgtg 72
DB 3 ATGTGCGAGCTGGAACGCAACATAGACCATATCAACACCTTCACCAATACTCTGTG 62

QY 73 aagctggggcaccacagaaacccctgaaccagggtgaattcaaaagctgtgtgcaaaagat 132
DB 63 AAGCTGGGGCACACCAGACACCTGAACAGGGGAATTCAAAAGAGCTGTGGAAAGAT 122

QY 133 ctgcgaattttctcaaaagagagataagaatgaaaggtcatatgacacatctagag 192
DB 123 CTGCAAAATTTTCTCAAGAAGAGATTAAGATGAAGGTCAATAGAACACATCATGGAG 182

QY 193 gacctggacacaatgacgaacaagcagctgagcttcgagaggtcatcatgtgtatggcg 252
DB 183 GACCTGGACACAATGACAGACAGCAGCTGAGCTTCGAGAGATTTTCATGCTGATGGCG 242

QY 253 aggtctaacttggtgctcccaagagaagatgcaagaggtgacagagggcctggccaacac 312
DB 243 AGGCTAACCTGGGCTCCACAGAGAAAGATGCACGAGGTGACGAGGGCCTGGCCACAC 302

QY 313 cataagcaggcctcggtggaggagcaccctctaa 345
DB 303 CATTAAGCCAGGCTCGGAGAGGCCACCCCTTA 335

RESULT 12
A12032 1754 bp DNA linear PAT 12-JAN-1994
LOCUS
DEFINITION PARTIAL Macrophage migration inhibition factor (MRP-14) from a
human Placenta or fetal liver cells (formula 6).
ACCESSION A12032
VERSION A12032.1 GI:490107
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1754)
AUTHORS Odink,K.G., Clerc,R., Cerletti,N., Brueggen,J., Tarcsay,L., Sorg,C.
and Wiesendanger,W.
TITLE Novel lymphokine related peptides
JOURNAL Patent: EP 0263072-A 18 06-APR-1988;
CIBA-GEIGY AG

FEATURES
source 1..1754
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/db_xref="taxon:9606"
gene 711..905
/gene="MRP-14"
CDS 711..905
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/db_xref="GI:490108"
/translation="KENKNEKVIHEIMEDLDTNADKQLSFEETIMLARLTWASHEKMGDEGPGHHHK
HEGDEGSHHKKRGIGEGTP"

AUTHORS Wang, M.-R., Xu, X., Cai, Y., Xu, H., Han, Y.-L., Xu, Z.-X. and Wu, M.
TITLE Human gene for migration inhibitory factor-related protein 14 (MRP14), variant allele

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4804)
AUTHORS Wang, M.-R., Xu, X., Cai, Y., Xu, H., Han, Y.-L., Xu, Z.-X. and Wu, M.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2000) National Laboratory of Molecular Oncology, Cancer Institute, CAMS, PUMC, Panjiayuan, Chaoyang Qu, Beijing 100021, China

FEATURES
source Location/Qualifiers
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 /db_xref="taxon:9606"
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 /gene="S100A9"
 /note="MRP14p"
 /codon_start=1
 /product="migration inhibitory factor-related protein 14 variant p"
 /protein_id="AAF62536.1"
 /db_xref="GI:7417327"
 /translation="MTCKMSQLERNIETIINTFHQYSVKLGHPDTLNGEPKELVRKD LQNLKKENKNEKYIEHIMEDLDINADKQLSFEFIMLMARLTWASHEKMHGDEGPG HHKPGEGEPTP"
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CDS
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BASE COUNT 1158 a 1317 c 1237 g 1092 t

ORIGIN

Query Match 57.1%; Score 197; DB 9; Length 4804;
 Best Local Similarity 100.0%; Pred. No. 1.3e-37;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 agaagagaataagaatgaaagtcataagaacacatcatgtgaggaacctggacacaatg 208
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Db 3794 AGAAGAGAAATGAAGATGAAGATGATGAACACATCATGTGAGAGACCTGACACAAATG 3853
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QY 209 cagacaagcagctgagcttcgagaggttcacatgctgattgagcagcctaaccctggcct 268
 |||||||
Db 3854 CAGACAGCAGCTGAGCTTCGAGAGTTCATCATGCTGATGGAGGCTAACCTGGGCT 3913
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QY 269 ccacagagaagatgacgagaggtgacgagggcctggtccaccacataagccaagcctcg 328
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Db 3914 CCCACGAGAAGATGCACGAGGTTGACGAGGGCCTGGCCACCACCATAGCCAGGCTCG 3973
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QY 329 gggagggaacccctaa 345
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Db 3974 GGGAGGGCACCCCTAA 3990

Search completed: September 10, 2002, 06:42:47
 Job time: 6403 sec

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Date: Sep 9, 2002 3:11 PM

About: Results were produced by the GenCore software, version 4.5,
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Search information block:

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/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-09-270-455-20			158.00	364.63	8.7e-13		92	92
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-08-794-000-2			151.00	348.09	7.4e-12		91	91
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-08-918-727-5			139.00	319.43	2.9e-10		92	92
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/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-07-987-272A-12			118.50	272.77	1.5e-07		97	97
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-08-918-727-7			111.00	251.46	1.5e-06		105	105
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-09-205-680A-6			109.50	248.29	2.4e-06		101	101
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-08-469-946-2			109.50	248.29	2.4e-06		101	101
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-07-987-272A-10			108.00	246.02	3.6e-06		89	89
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-08-918-727-1			105.50	238.57	8.2e-06		103	103
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-09-205-680A-1			103.50	234.65	1.5e-05		95	95

/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-08-918-727-3 + 101.50 229.57 2.7e-05 98
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-09-205-680A-3 + 101.50 229.57 2.7e-05 98
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-09-048-889-11 + 101.50 229.57 2.7e-05 98
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-08-056-200-94 + 98.00 190.69 0.0002 1898
/cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-08-800-644-94 + 98.00 190.69 0.0002 1898

seq_name: /cgn2_6/p/ptodata/2/iaa/5A.COMB.pdp:US-07-987-272A-7

seq_documentation_block:

Sequence 7, Application US/07987272A

Patent No. 5731166

GENERAL INFORMATION:

APPLICANT: Geczy, C., Simpson, R. J. and Lackmann, M

TITLE OF INVENTION: No. 5731166el Chemoclastic Factor

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESS: Cushman Darby & Cushman

STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower

CITY: Washington

STATE: D. C.

COUNTRY: USA

ZIP: 20005-3918

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/987, 272A

FILING DATE: 05-MAR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK 2127

FILING DATE: 05-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK 4463

FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: Brinkman, David W

REGISTRATION NUMBER: 20,817

REFERENCE/DOCKET NUMBER: DMB/1925/200259

TELEPHONE: 202-822 3000

TELEFAX: 202-822 0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 93 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-987-272A-7

alignment_scores:

Quality: 485.00

Ratio: 5.215

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

US-09-806-382A-1 x US-07-987-272A-7

Align seg 1/1 to: US-07-987-272A-7 from: 1 to: 93

1 ATGTGACCGAGCGGGAAGCCCTGAACCTTCATCCAGCGCTACCA 50
|||||
1 MetLeuTrnGluLeuGlnAlaLeuAsnSerIleIleAspValTyrH1 17
51 CAAGTACTCCCTGATTAAGGGGAATTTCATGCCGCTACAGGAGTACC 100
|||||
17 slsYsrSerLeuLeuLeuysGlnAsnPhenHisAlaValTyrArgspAspL 34

```
101 TGAAGAAATTCGTAGAGACCGAGTCTCTCAGTATATACAGAAAAAGGT 150
|||||
34 eulysylsleuleuGlutThnGlucysProglIntYrIleargLysGly 50
|||||
151 GCAGAGCTGTGTTCAAGAGATTGGATATCACACTGATGTCAGTTAA 200
|||||
51 AlaAspValItrPheLysGluLeuAspIleAsnThrAspLysAlaValas 67
|||||
201 CTTCCAGAGATTCTCATTTCTGTGATTAAGATGGCGTGCGAGCCACA 250
|||||
67 nPhgIngluPheLeuIleLeuValIleLysMetGlyValAlaAlaHisL 84
|||||
251 AAAAAAGCCATGAAGAACCCACAAAGAG 279
|||||
84 yLysSerHisGluGluSerHisLysGlu 93

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-07-987-272A-16

seq_documentation_block:
: Sequence 16, Application US/07987272A
: Patent No. 5731166
: GENERAL INFORMATION:
: APPLICANT: Gezey, C., Simpson, R. J. and Lackmann, M
: TITLE OF INVENTION: No. 5731166el Chemolactic Factor
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cushman Darby & Cushman
: STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower
: CITY: Washington
: STATE: D. C.
: COUNTRY: USA
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/987,272A
: FILING DATE: 05-MAR-1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: AU PK 2127
: FILING DATE: 05-FEB-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: AU PK 4463
: FILING DATE: 05-SEP-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Blinkman, David W
: REGISTRATION NUMBER: 20,817
: REFERENCE/DOCKET NUMBER: DMB/1925/200259
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-861 3000
: TELEFAX: 202-822 0944
: TELETYPE: 6714627 CUSH
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 93 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-987-272A-16

alignment_scores:
Quality: 485.00 Length: 93
Ratio: 5.215 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382A-1 x US-07-987-272A-16 ..
Align seg 1/1 to: US-07-987-272A-16 from: 1 to: 93
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1 ATGTTGACCGAGCTGGAGAAAGCCTTGAACCTATATCATCGACGCTACCA 50
|||||
1 MetLeuThriGluLeuGluLysAlaLeuAsnSerIleIleAspValItryH 17
|||||
51 CAAGTACTCCCTGATTAAGGGGAATTCATGCCGCTCTACAGGAGATGACC 100
|||||
17 sLysYrSerLeuIleLysGlyAsnPhenHisAlaValItryArgAspAspL 34
|||||
101 TGAAGAAATTCGTAGAGACCGAGTCTCTCAGTATATACAGAAAAAGGT 150
|||||
34 eulysylsleuleuGlutThnGlucysProglIntYrIleargLysGly 50
|||||
151 GCAGAGCTGTGTTCAAGAGATTGGATATCACACTGATGTCAGTTAA 200
|||||
51 AlaAspValItrPheLysGluLeuAspIleAsnThrAspLysAlaValas 67
|||||
201 CTTCCAGAGATTCTCATTTCTGTGATTAAGATGGCGTGCGAGCCACA 250
|||||
67 nPhgIngluPheLeuIleLeuValIleLysMetGlyValAlaAlaHisL 84
|||||
251 AAAAAAGCCATGAAGAACCCACAAAGAG 279
|||||
84 yLysSerHisGluGluSerHisLysGlu 93

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-385-241-1

seq_documentation_block:
: Sequence 1, Application US/08385241
: Patent No. 5776348
: GENERAL INFORMATION:
: APPLICANT: Seleniut Ph.D., Jeremy D.
: APPLICANT: Orme-Johnson Ph.D., William H.
: APPLICANT: Dretler M.D., Stephen P.
: APPLICANT: Asakura M.D., Hirotsuka
: TITLE OF INVENTION: SYSTEM AND METHOD FOR INHIBITING
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Choate, Hall & Stewart
: STREET: 53 State Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109-2891
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/385,241
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Herschbach Ph.D., Brenda M.
: REGISTRATION NUMBER: P-39,223
: REFERENCE/DOCKET NUMBER: 492611-000 (MIT6915)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 248-5175
: TELEFAX: (617) 248-4000
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 93 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: IMMEDIATE SOURCE:
: CLONE: hmrp-8 protein
: US-08-385-241-1
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alignment_scores:

Quality: 485.00 Length: 93
Ratio: 5.215 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-1 x US-08-385-241-1 ..

Align seg 1/1 to: US-08-385-241-1 from: 1 to: 93

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1  AAGTTGACCGAGCTGGAGAAAGCCTTGACTATCATGACGCTTACCA 50
|||||
17 MetLeuThrGluLeuGluLysAlaLeuAsnSerIleIleLeuValTyrHI 17
51 CAAGTACTCTCCGTGATAAGGGAATTTCCATGCTCTACAGGAGTAC 100
|||||
17 sLysTyrSerIleuIleLysGlyAsnPhenIleAlaValTyrAspAspL 34
101 TGAAGAAATTTGCTAGACCGAGTGTCTCAGTATATCAGAAAAAGGT 150
|||||
34 euLysLysLeuLeuGluThrGluLysProGlnTyrIleArgLysLysGly 50
151 GCAGACGCTGTGCTCAAGAGTTGGATATCAACACTGATGTGAGTTAA 200
|||||
51 AlaAspValTyrPhenylsGluLeuAspIleAsnThrAspGlyAlaValAs 67
201 CTTCCAGAGTTCCTCATCTGCTGATTAAGATGGCGCTGACGCCACCA 250
|||||
67 nPhenGlnLysPheLeuIleLeuValIleLysMetGlyAlaAlaIleHisL 84
251 AAAAAAGCCATGAGAAAGCCACAAAGAG 279
|||||
84 yslSerHisGluGluSerHisLysGlu 93
```

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-07-987-272A-14

seq_documentation_block:

; Sequence 14, Application US/07987272A
; Patent No. 5731166
; GENERAL INFORMATION:
; APPLICANT: Geczy, C., Simpson, R. J. and Lackmann, M
; TITLE OF INVENTION: No. 5731166el Chemotactic Factor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman Darby & Cushman
; STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,272A
; FILING DATE: 05-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 2127
; FILING DATE: 05-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 4463
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brinkman, David W
; REGISTRATION NUMBER: 20,817
; REFERENCE/DOCKET NUMBER: DMB/1925/200259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861 3000

; TELEFAX: 202-822 0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 89 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-987-272A-14

alignment_scores:

Quality: 295.00 Length: 89
Ratio: 3.734 Gaps: 0
Percent Similarity: 88.764 Percent Identity: 58.427

alignment_block:

US-09-806-382A-1 x US-07-987-272A-14 ..

Align seg 1/1 to: US-07-987-272A-14 from: 1 to: 89

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1  AAGTTGACCGAGCTGGAGAAAGCCTTGACTATCATGACGCTTACCA 50
|||||
1 MetProSerGluLeuGluLysAlaLeuSerAsnLeuIleAspValTyrHI 17
51 CAAGTACTCTCCGTGATAAGGGAATTTCCATGCTCTACAGGAGTAC 100
|||||
17 sAsnTyrSerAsnIleGlnGlyAsnHisAlaLeuTyrLysAsnAsp 34
101 TGAAGAAATTTGCTAGACCGAGTGTCTCAGTATATCAGAAAAAGGT 150
|||||
34 helLysMetValThrThrGluLysProGlnPheValGlnAsnIleAsn 50
151 GCAGACGCTGTGCTCAAGAGTTGGATATCAACACTGATGTGAGTTAA 200
|||||
51 IleGluAsnLeuPheArgGluLeuAspIleAsnSerAspAsnAlaIleAs 67
67 nPhenGluGluPheLeuAlaMetValIleLysValGlyAlaIleSerHisL 84
251 AAAAAAGCCATGAGAA 267
|||||
84 ysaSpSerHisLysGlu 89
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seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-07-987-272A-1

seq_documentation_block:

; Sequence 1, Application US/07987272A
; Patent No. 5731166
; GENERAL INFORMATION:
; APPLICANT: Geczy, C., Simpson, R. J. and Lackmann, M
; TITLE OF INVENTION: No. 5731166el Chemotactic Factor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman Darby & Cushman
; STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,272A
; FILING DATE: 05-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 2127
; FILING DATE: 05-FEB-1990

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 4463
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brinkman, David W
; REGISTRATION NUMBER: 20,817
; REFERENCE/DOCKET NUMBER: DWB/1925/200259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861 3000
; TELEFAX: 202-822 0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 88 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-987-272A-1
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alignment_scores:
  Quality: 293.00      Length: 87
  Ratio: 3.756         Gaps: 0
  Percent Similarity: 89.655      Percent Identity: 58.621
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alignment_block:
US-09-806-382A-1 x US-07-987-272A-1 ..
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Align seg 1/1 to: US-07-987-272A-1 from: 1 to: 88
```

```

7 ACCGAGCTGAGAGAAAGCCTTGAACTCTATCATGACGCTGCACACAAGTA 56
  :::::::::::::::::::::::::::::::::::::::::::::::::::::::
2 SerGluLeuGluLysAlaLeuSerAsnLeuIleAspValTyrHisAsnTy 18
57 CTCCTGATAAAGGGAATTTCCATGCCCTCTACAGAGGATGACCTGACAGA 106
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
18 rSerAsnIleGlnGlyAsnHisAlaLeuTyrLysAsnAspPheLysL 35
107 AATTGCTAGACGACGAGTGTCTCAGTATATCAGAGAAAGGCTGCAGAC 156
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
35 ySmeValThrThrGluCysProGlnPheValGlnAsnIleAsnIleGlu 51
157 GTCTGCTCAAGAGCTGGATATCAACACTGATGGTGCAGTTAACTTCCA 206
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
52 AsnLeuPheArgGluLeuAspIleAsnSerAspAsnAlaIleAsnPheG 68
207 GGAGTTCTCATTTCTGGTGATTAAGATGGCGCTGCAGCCCAAAAAA 256
  :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 uGlnPheLeuAlaMetValIleLysValGlyAlaIleAsnHisLysAsp 85
257 GCCATGAGAA 267
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
85 erHisLysGlu 88
```

```

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-07-987-272A-17
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seq_documentation_block:
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; Sequence 17, Application US/07987272A
; Patent No. 5731166
; GENERAL INFORMATION:
; APPLICANT: Geecy, C., Simpson, R. J. and Lackmann, M
; TITLE OF INVENTION: No. 5731166el Chemotactic Factor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman Darby & Cushman
; STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,272A
; FILING DATE: 05-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 2127
; FILING DATE: 05-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 4463
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brinkman, David W
; REGISTRATION NUMBER: 20,817
; REFERENCE/DOCKET NUMBER: DWB/1925/200259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861 3000
; TELEFAX: 202-822 0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-987-272A-17
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alignment_scores:
  Quality: 247.00      Length: 75
  Ratio: 3.687         Gaps: 0
  Percent Similarity: 89.333      Percent Identity: 57.333
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alignment_block:
US-09-806-382A-1 x US-07-987-272A-17 ..
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Align seg 1/1 to: US-07-987-272A-17 from: 1 to: 76
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```

7 ACCGAGCTGAGAGAAAGCCTTGAACTCTATCATGACGCTGCACACAAGTA 56
  :::::::::::::::::::::::::::::::::::::::::::::::::::::::
2 SerGluLeuGluLysAlaLeuSerAsnLeuIleAspValTyrHisAsnTy 18
57 CTCCTGATAAAGGGAATTTCCATGCCCTCTACAGAGGATGACCTGACAGA 106
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
18 rSerAsnIleGlnGlyAsnHisAlaLeuTyrLysAsnAspPheLysL 35
107 AATTGCTAGACGACGAGTGTCTCAGTATATCAGAGAAAGGCTGCAGAC 156
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
35 ySmeValThrThrGluCysProGlnPheValGlnAsnIleAsnIleGlu 51
157 GTCTGCTCAAGAGCTGGATATCAACACTGATGGTGCAGTTAACTTCCA 206
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
52 AsnLeuPheArgGluLeuAspIleAsnSerAspAsnAlaIleAsnPheG 68
207 GGAGTTCTCATTTCTGGTGATTAAG 231
  :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 uGlnPheLeuAlaMetValIleLys 76
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```

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seq_documentation_block:
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; Sequence 2, Application US/08200016
; Patent No. 5614397
; GENERAL INFORMATION:
; APPLICANT: Weissman, Irving
; APPLICANT: Lagasse, Eric
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR MODULATING
; TITLE OF INVENTION: APOPTOSIS IN HEMATOLYMPHOID CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,016
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: 06037/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-5277
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-200-016-2

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alignment_scores:
    Quality: 245.00      Length: 47
    Ratio: 5.213        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

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alignment_block:

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US-09-806-382A-1 x US-08-200-016-2
Align seg 1/1 to: US-08-200-016-2 from: 1 to: 47

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1 ATGTTGACGAGCTGAGAGAAAGCTTGAACCTATCATGACGCTACCA 50
  |||||||
1 MetleuThnGlueGluLysAlaLeuAsnSerIleIleAspValTyrHi 17
17 slySTYrSerIleuIleLysGlyAsnPhelHisAlaValTyrArgAspAsp 34
51 CAAGTACTCCGTGATTAAGGGAATTTCATGCCGTCTACAGGATGACC 100
  |||||||
17 slySTYrSerIleuIleLysGlyAsnPhelHisAlaValTyrArgAspAsp 34
101 TGAAGAAATTGCTAGAGACCGAGTGTCTCATATATGACG 141
  |||||||
34 euLysLysLeuLeuGluThrGluCysProGluIleTyrIleArg 47

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-200-016-3
seq_documentation_block:
; Sequence 3, Application US/08200016
; Patent No. 5614397
; GENERAL INFORMATION:
; APPLICANT: Weissman, Irving
; APPLICANT: Lagasse, Eric
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR MODULATING
; TITLE OF INVENTION: APOPTOSIS IN HEMATOLYMPHOID CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,016
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: 06037/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-5277
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-200-016-3

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alignment_scores:
    Quality: 240.00      Length: 46
    Ratio: 5.217        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

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alignment_block:

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US-09-806-382A-1 x US-08-200-016-3
Align seg 1/1 to: US-08-200-016-3 from: 1 to: 46

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142 AAAAAGGTGACGAGCTGTGTTCAAGAGTTGATATCAACTGATGG 191
  |||||||
1 LysLysGlyAlaAspValTyrPhelGluLeuAspIleAsnThrAsp 17
192 TGCAGTTAACTCCAGAGATTCTCATTTGGTGATTAAGATGGCGTGG 241
  |||||||
17 yAlaValAsnPhelGluLeuLeuValIleLysMetClyValA 34
242 CAGCCCAAAAAAGCCATGAAGAAAGCCCAAGAG 279
  |||||||
34 laAlaHisLysLysSerHisGluLeuSerHisLysGlu 46

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-056-200-101
seq_documentation_block:
; Sequence 101, Application US/08056200
; Patent No. 5616500
; GENERAL INFORMATION:
; APPLICANT: Steinert, Peter M.
; APPLICANT: Lee, Seung-Chul
; APPLICANT: Kim, In-Gyu
; APPLICANT: Chung, Soo-Il
; APPLICANT: Park, Sang-Chul
; TITLE OF INVENTION: Trichothyalin and Transglutaminase-3 and
; TITLE OF INVENTION: Methods of Using Same
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/056,200

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; FILING DATE: 30-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH054.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-056-200-101

alignment_scores:
  Quality: 236.00      Length: 45
  Ratio: 5.244        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-806-382A-1 x US-08-056-200-101  ...
Align seg 1/1 to: US-08-056-200-101 from: 1 to: 45

7 ACCGAGCTGAGAAAGCCTTGAACTATATCAGCTACCAACAAGTA 56
|||||
1 ThnglueglulysAlaleuanserilleaspvaltyrhisysty 17
|||||
57 CTCCTGATRAAGGGAATTCATCCGCTACAGGAGTACCTGAAGA 106
|||||
17 rserleuilelysglyasnphetisAlavaltyrtaqaspaspleuylsL 34
|||||
107 AATGCTAGAGACCGAGTGCTCTCACTATATACAG 141
|||||
34 yslenuelugluthrglucysProglntyrileary 45

seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-800-644-101

seq_documentation_block:
; Sequence 101, Application US/08800644
; Patent No. 5958752
; GENERAL INFORMATION:
; APPLICANT: Steinert, Peter M.
; APPLICANT: Lee, Seung-Chul
; APPLICANT: Kim, In-Gyu
; APPLICANT: Chung, Soo-Il
; APPLICANT: Park, Sang-Chul
; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,644
; FILING DATE: 14-FEB-1997

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/056,200
; FILING DATE: 30-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH054.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-800-644-101

alignment_scores:
  Quality: 236.00      Length: 45
  Ratio: 5.244        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
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7 ACCGAGCTGAGAAAGCCTTGAACTATATCAGCTACCAACAAGTA 56
|||||
1 ThnglueglulysAlaleuanserilleaspvaltyrhisysty 17
|||||
57 CTCCTGATRAAGGGAATTCATCCGCTACAGGAGTACCTGAAGA 106
|||||
17 rserleuilelysglyasnphetisAlavaltyrtaqaspaspleuylsL 34
|||||
107 AATGCTAGAGACCGAGTGCTCTCACTATATACAG 141
|||||
34 yslenuelugluthrglucysProglntyrileary 45

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-056-200-108

seq_documentation_block:
; Sequence 108, Application US/08056200
; Patent No. 5616500
; GENERAL INFORMATION:
; APPLICANT: Steinert, Peter M.
; APPLICANT: Lee, Seung-Chul
; APPLICANT: Kim, In-Gyu
; APPLICANT: Chung, Soo-Il
; APPLICANT: Park, Sang-Chul
; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-056-200-108

alignment_scores:
Quality: 213.00 Length: 41
Ratio: 5.195 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382a-1 x US-08-056-200-108 ..

Align seg 1/1 to: US-08-056-200-108 from: 1 to: 41

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|||||
1 LysLysGclYAlaAspValTrpPheLysGluLeuAspIleAsnThrAspG1 17
192 TGCAGTTAACTTCCAGAGTCTCATTTGTTGATTAAGATGGCGCTGG 241
|||||
17 yAlaValAsnPhelnglnuPheLeuIleLeuValIleLysMetGlyValA 34
242 CAGCCCAAAAAAAGCCATGAA 264
|||||
34 laAlaHisLysLysSerHisGlu 41

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-800-644-108

seq_documentation_block:

; Sequence 108, Application US/08800644
; Patent No. 5958752
; GENERAL INFORMATION:
; APPLICANT: Steinert, Peter M.
; APPLICANT: Lee, Seung-Chul
; APPLICANT: Kim, In-Gyu
; APPLICANT: Chung, Soo-Il
; TITLE OF INVENTION: Trichothyalin and Transglutaminase-3 and
; TITLE OF INVENTION: Methods of Using Same
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,644

FILING DATE: 14-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/056,200
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-800-644-108

alignment_scores:
Quality: 213.00 Length: 41
Ratio: 5.195 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382a-1 x US-08-800-644-108 ..

Align seg 1/1 to: US-08-800-644-108 from: 1 to: 41

142 AAAAAGGTGCAGACGTGTGTTCAAGAGTTGATATCAACACTGATGG 191
|||||
1 LysLysGclYAlaAspValTrpPheLysGluLeuAspIleAsnThrAspG1 17
192 TGCAGTTAACTTCCAGAGTCTCATTTGTTGATTAAGATGGCGCTGG 241
|||||
17 yAlaValAsnPhelnglnuPheLeuIleLeuValIleLysMetGlyValA 34
242 CAGCCCAAAAAAAGCCATGAA 264
|||||
34 laAlaHisLysLysSerHisGlu 41

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-568-310D-19

seq_documentation_block:

; Sequence 19, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1


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seq_name: /cgn2_6/protodata/2/iaa/SB_COMB.pep:US-08-568-310D-20
seq_documentation_block:
; Sequence 20, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564(both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3352
; TELEFAX: (212)953-3350
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 20:
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
; US-08-568-310D-20

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Quality: 158.00 Length: 96
Ratio: 2.508 Gaps: 2
Percent Similarity: 65.625 Percent Identity: 38.542

alignment_block:
US-09-806-382A-1 x US-08-568-310D-20 ..

Align seg 1/1 to: US-08-568-310D-20 from: 1 to: 92

4 TTGACGAGGTGAGAAAGCCTTGAACTATATCATGACGCTTACACAA 53
:::|||||::: |||::: |||:::
1 Methrlysluenglunlsluengllyllevalsnllephtsgl 17
:::|||||::: |||::: |||:::
54 GTACTCCGTGATAAGGGGAATTCCATGCCGCTTACAGGATGACCTGA 103
:::|||||::: |||::: |||:::
17 ntyrservalarglysgllylspheasprtlleuserlysglygluleul 34
:::|||||::: |||::: |||:::
104 AGAAATTGCTAGAGACCGAGTGTCTCAGTATATCAGG..... 141

```

```

||:||||| |||::: |||:::
34 ysglnleuethrlysgluleualasnthrilleysanlleysasp 50
142 AAAAAGGTCGACAGCTGTGTCMAAGAGTTGATATACACCTGATG 191
||| ||| |||::: ||| |||
51 lysalavallleasplullepneinglyleuaspalaasnlnaspl 67
192 TGCAGTTAACTTCAGAGATTCCATCTGTGATGAAGATGGCGGTG 241
||:||||| |||::: |||:::
67 ugnlvalasprhcglnsluphetleuserleual.....Alai 80
242 CAGCCCACAAAAAAGCCATGAAGAAAGCCACAAAGAG 279
||| ||| |||::: |||:::
80 lealaleuylsalaalaalnstyrlsthrnlstlysglu 92

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4

OM of: US-09-806-382a-1 to: PIR_71:* out_format : pfs
Date: Sep 9, 2002 3:12 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-O=/cgn2_1/USPTO.spool/US09806382/runat_09092002_143848_15421/app.query.fasta_1.752
-DB=PIR_71 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOCL=0.000 -LOOEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELDP=6.000
-DELXRT=7.000 -START=1 -MATRIX=blonum62 -TRANS=human40.cdt
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-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
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Search information block:

Query: US-09-806-382a-1
Query length: 282
Database: PIR_71:*
Database sequences: 283138
Database length: 96089334
Search time (sec): 60.920000

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Sequence	+	485.00	1040.00	93	calgranulin A [validated] - human
PIR1:BNHCF	+	320.00	684.67	89	calgranulin A - rat
PIR1:BNH65	+	295.00	630.77	89	calgranulin A - mouse
PIR1:156163	+	170.00	368.36	41	calcium-binding protein MRP-8 -
PIR2:B42628	+	158.00	335.05	92	S-100 calcium-binding protein A1
PIR2:CA4712	+	154.50	324.96	122	calgranulin B - bovine (fragment
PIR2:524146	+	154.00	326.17	95	S-100 protein P - human
PIR2:524106	+	151.00	320.10	91	calgranulin c - pig
PIR1:BNH01A	+	147.00	311.18	94	S-100 protein alpha chain - bovi
PIR1:BNH01B	+	145.00	306.87	94	S-100 protein alpha chain - huma
PIR1:BNH01C	+	139.00	294.13	92	S-100 protein beta chain [valida
PIR2:A48015	+	139.00	294.13	92	S-100 protein beta chain [valida
PIR2:A26577	+	138.00	291.97	92	S-100 protein beta chain - mouse
PIR1:BNH01B	+	137.00	289.92	91	S-100 protein beta chain - rat
PIR1:BNH01B	+	134.00	283.05	95	S-100 protein alpha chain - bovi
PIR1:BNH01B	+	133.50	280.31	114	calgranulin B [validated] - hum
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PIR1:BNH01B	+	130.50	273.92	113	calgranulin B - rat
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PIR2:BNH01B	+	124.00	260.93	101	calvasculin - mouse
PIR1:BNH01B	+	122.00	256.53	102	calvasculin - rabbit
PIR2:BNH01B	+	121.00	254.47	101	calvasculin - rat
PIR2:BNH01B	+	120.50	252.61	110	S-100 calcium-binding protein A
PIR1:BNH01B	+	119.50	253.48	79	calcium-binding protein, intesti
PIR2:A48188	+	118.50	249.35	98	S-100 calcium-binding protein A2
PIR1:BNH01B	+	115.50	244.86	79	calcium-binding protein, intesti
PIR2:A48118	+	114.50	224.29	591	proliferatin - human (fragment)
PIR2:A48118	+	114.00	229.23	306	major epidermal calcium-binding
PIR1:BNH01B	+	113.00	238.27	90	calcylin - rabbit
PIR1:BNH01B	+	112.50	238.39	79	calcium-binding protein, intesti
PIR1:BNH01B	+	112.00	236.51	97	calpactin I light chain - chick
PIR2:BNH01B	+	112.00	235.25	99	S-100 protein, lung - bovine
PIR2:BNH01B	+	111.00	232.55	105	calcium-binding protein S100C -
PIR1:BNH01B	+	110.00	231.81	90	calgizarrin - human
PIR1:BNH01B	+	110.00	206.65	1407	calcylin - human
PIR1:BNH01B	+	109.50	229.67	90	calcylin - rat
PIR2:BNH01B	+	109.00	229.65	101	calcylin [validated] - human
PIR2:BNH01B	+	108.00	227.60	89	calcylin - mouse

seq_name: PIR1:BNH01B

seq_documentation_block:

calgranulin A [validated] - human

M:Alternate names: calcium-binding protein MRP-8; cystic fibrosis-associated antigen

N:MRP-8; MRP-related protein 8k chain; oncodevelopmental protein; S-100 calcium-bindin

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence_revision 07-Oct-1994 #text_change 08-Dec-2000

C:Accession: A31848; S00705; S13454; A29764; A60911; A61082; C54327; A44111; S53791

R:Tagase, E.; Clerc, R.G.

Mol. Cell. Biol. 8, 2402-2410, 1988

A:Title: Cloning and expression of two human genes encoding calcium-binding proteins

A:Reference number: A93102; MUID:86302148

A:Accession: A31848

A:Molecule type: DNA

A:Residues: 1-93 <LAG>

A:Cross-references: GB:M21005; NID:g34772; PIDN:CAA36327.1; PID:g386959

R:Odink, K.; Cerletti, N.; Brueggemann, J.; Clerc, R.G.; Tarses, L.; Zwadlo, G.; Gerhar

Nature 330, 80-82, 1987

A:Title: Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis

A:Reference number: S00667; MUID:88039099

A:Accession: S00705

A:Molecule type: mRNA

A:Residues: 1-93 <ODI>

A:Cross-references: EMBL:X06234; NID:g34772; PIDN:CAA29580.1; PID:g34773

A:Note: Part of this sequence, including the amino end of the mature protein, was con

R:Schaefer, T.; Sachse, G.E.; Gassen, H.G.

Biol. Chem. Hoppe-Seyler 372, 1-4, 1991

A:Title: The calcium-binding protein MRP-8 is produced by human pulmonary tumor cells

A:Reference number: S13454; MUID:91248411

A:Accession: S13454

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-93 <SCH>

R:Dorin, J.R.; Novak, M.; Hill, R.E.; Brock, D.J.H.; Secher, D.S.; van Heyningen, V.

Nature 326, 614-617, 1987

A:Title: A clue to the basic defect in cystic fibrosis from cloning the CF antigen ge

A:Reference number: A29764; MUID:87173041

A:Accession: A29764

A:Molecule type: mRNA

A:Residues: 1-78; 'AMPTKAKKAKRS' <DOR>

A:Cross-references: EMBL:Y00278; NID:g29887; PIDN:CAA68390.1; PID:g29888

A:Note: the differences after residue 78 are due to a frameshift

R:Andersen, K.B.; Sletten, K.; Bernitz, H.B.; Dale, I.; Brandtzaeg, P.; Uellum, E.;

Scand. J. Immunol. 28, 241-245, 1988

A:Title: The leucocyte LI protein: identity with the cystic fibrosis antigen and the

A:Reference number: A60911; MUID:88321575

A:Accession: A60911

A:Molecule type: protein

A:Residues: 1-53, 'X', 55-56, 'X', 58-59, 78-84, 'X', 86-89 <AND>

R:Tobe, T.; Murakami, K.; Tomita, M.; Nozawa, R.

Chem. Pharm. Bull. 37, 1576-1580, 1989

A:Title: Amino acid sequences of 6088 antigens induced in HU-60 cells by 1,25-dihydro

A:Reference number: A61082; MUID:89376638

A:Accession: A61082

A:Molecule type: protein

A:Residues: 1-27; 29-33; 40-46; 58-69; 71-81, 'S', 83-84, 'S' <TOB>

A:Experimental source: chronic myeloid leukemic cell line

R:Madson, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Dejgaard, K.; Olsen, E.; Kill

J. Invest. Dermatol. 97, 701-712, 1991

A:Title: Molecular cloning, occurrence, and expression of a novel partially secreted

A:Accession: C54327

A:Molecule type: protein

A:Residues: 'X', 38-47; 50-53, 'X', 55-56 <MAD>

R:Remarchand, P.; Vaglio, M.; Manuel, J.; Markert, M.

J. Biol. Chem. 267, 19379-19382, 1992
A:Title: Translocation of a small cytosolic calcium-binding protein (MRP-8) to plasma me
A:Reference number: A44111; MUID:92406885
A:Accession: A44111
A:Molecule type: protein
A:Residues: 1-25 <LEMB>
A:Experimental source: zymosan-activated neutrophils
A:Note: Sequence extracted from NCBI backbone (NCBIP:113895)
R:Nakai, M.; Ishikawa, M.; Hamada, Y.; Sugano, S.
Biol. Chem. Hoppe-Seyler 375, 789-792, 1994
A:Title: Isolation of an ascitic oncodevelopmental protein exhibiting high sequence hom
A:Reference number: S53791; MUID:95209785
A:Accession: S53791
A:Molecule type: protein
A:Residues: 1-16, 'X', 18-20 <NAN>
C:Comment: Concentrations of this protein, a product of normal and leukemic granulocytes
C:Comment: This protein can bind two calcium ions per molecule with an affinity similar
C:Genetics:
A:Gene: GDB:S100A8; CAGA; CPAG
A:Cross-references: GDB:120569; OMIM:123885
A:Map position: 1q21-1q21
A:Introns: 47/73
A:Note: the first intron occurs before the initiator codon
C:Complex: homodimer; heterodimer and higher complexes with calgranulin B (see PIR:B3184
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; cytokine; EF hand; heterodimer; homodimer; inflammation
F:1-93/Product: calgranulin A status experimental <MAT>
F:7-41/Domain: calmodulin repeat homology <EP1>
F:46-78/Domain: calmodulin repeat homology <EP2>

alignment_scores:
Quality: 485.00 Length: 93
Ratio: 5.215 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-1 x BCHUCF ..

Align seg 1/1 to: BCHUCF from: 1 to: 93

```
1  ATGTTGACCGAGCTGGAGAAAGCCTTGAACCTATCATCGAGCTTACCA 50
|||||
1  MetcAlaThrGluLeuGlnLysAlaLeuAsnSerIleIleAspValTyrHl 17
51  CAAGTACTCCCTGATTAAGGGAATTTCCATCCGCTACAGGAGTACCC 100
|||||
17  slysrYrSerIleuIleLysGlyAsnPhenHisAlaValTyrArgAspAsp 34
34  eulYsLysLeuLeuGlnThrGlnLysProGlnTyrIleArgLysLysGly 50
101  TGAAGAAATTGCTAGAGACCGAGTGTCTCATATATCAGAAAAAGGT 150
|||||
34  eulYsLysLeuLeuGlnThrGlnLysProGlnTyrIleArgLysLysGly 50
151  GCAGACGTCCTGTTCAAGAGTTGGATATCACACGATGATGGCAGTTAA 200
|||||
51  AlaAspValTyrPheLysGlnLeuAspIleAsnThrAspGlyAlaValAs 67
201  CTTCCAGAGTTCCTCATCTGTGATTAAGATGGCGCGGAGCCACACA 250
|||||
67  nPhedInGlnPheLeuIleLeuValIleLysMetGlyAlaAlaIleHsl 84
251  AAAAAAGCCATGAGAAAGCCACAAAGAG 279
|||||
84  yLysSerHisGlnLysSerHisLysGln 93
```

seq_name: p1r1:JN0685

seq_documentation_block:

calgranulin A - rat
N:Alternate names: calcium-binding protein MRP-8; macrophage migration inhibitory factor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 23-May-1997 #text_change 22-Jun-1999
C:Accession: JN0685

R:Imamiuchi, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.
Biochem. Biophys. Res. Commun. 194, 819-825, 1993
A:Title: Expression and cloning of migration inhibitory factor-related protein (MRP) 8
A:Reference number: JN0685; MUID:93343942
A:Accession: JN0685
A:Molecule type: mRNA
A:Residues: 1-89 <IMA>
A:Cross-references: GB:LI8891; NID:g349548; PIDN:AAA41637.1; PID:g349549
A:Experimental source: strains LEW/N and F344/N
C:Comment: This protein has a role in susceptibility to SCW-induced chronic disease.
C:Genetics:
A:Gene: MRP8
C:Complex: homodimer; heterodimer and higher complexes with calgranulin B
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; cytokine; EF hand; heterodimer; homodimer; inflammation
F:7-41/Domain: calmodulin repeat homology <EP1>
F:46-78/Domain: calmodulin repeat homology <EP2>

alignment_scores:
Quality: 320.00 Length: 89
Ratio: 3.951 Gaps: 0
Percent Similarity: 91.011 Percent Identity: 62.921

alignment_block:

US-09-806-382A-1 x JN0685 ..

Align seg 1/1 to: JN0685 from: 1 to: 89

```
1  ATGTTGACCGAGCTGGAGAAAGCCTTGAACCTATCATCGAGCTTACCA 50
|||||
1  MetcAlaThrGluLeuGlnLysAlaLeuAsnSerIleIleGluValTyrHl 17
51  CAAGTACTCCCTGATTAAGGGAATTTCCATCCGCTACAGGAGTACCC 100
|||||
17  sasnYrSerGlyIleLysGlyAsnHisAlaLeuTyrArgAspAsp 34
34  heargLysMetValThrThrGlnLysProGlnPheValGlnsnLysAsn 50
101  TGAAGAAATTGCTAGAGACCGAGTGTCTCATATATCAGAAAAAGGT 150
|||||
34  heargLysMetValThrThrGlnLysProGlnPheValGlnsnLysAsn 50
151  GCAGACGTCCTGTTCAAGAGTTGGATATCACACGATGATGGCAGTTAA 200
|||||
51  ThrGlnSerLeuPheLysGlnLeuAspValAsnSerAspAsnAlaIleAs 67
201  CTTCCAGAGTTCCTCATCTGTGATTAAGATGGCGCGGAGCCACACA 250
|||||
67  nPhedInGlnPheLeuAlaLeuValIleArgValGlyAlaAlaIleHsl 84
251  AAAAAAGCCATGAGAA 267
|||
84  yAspSerHisLysGln 89
```

seq_name: p1r1:I56163

seq_documentation_block:

calgranulin A - mouse
N:Alternate names: calcium-binding protein MRP-8; CP-10 chemotactic protein; macroph
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 23-May-1997 #text_change 22-Jun-1999
C:Accession: I56163; A42488
R:Lackmann, M.; Rajasekariah, P.; Iismaa, S.E.; Jones, G.; Cornish, C.J.; Hu, S.; Slm
J. Immunol. 150, 2981-2991, 1993
A:Title: Identification of a chemotactic domain of the pro-inflammatory S100 protein
A:Reference number: I56163; MUID:93203618
A:Accession: I56163
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <LACI>
A:Cross-references: GB:S57123; NID:g298706; PIDN:AMB25840.1; PID:g298707
R:Lackmann, M.; Cornish, C.J.; Simpson, R.J.; Moritz, R.L.; Geczy, C.L.
J. Biol. Chem. 267, 7499-7504, 1992
A:Title: Purification and structural analysis of a murine chemotactic cytokine (CP-10

```

A:Reference number: A42488; MUID:92218405
A:Accession: A42488
A:Molecule type: protein
A:Residues: 2-77 <LAC2>
A>Note: sequence extracted from NCBI backbone (NCBIP:94068)
C:Genetics:
A:Gene: MRP8
C:Complex: homodimer; heterodimer and higher complexes with calgranulin B
C:Superfamily: S-100 protein; calmodulin repeat homologs
C:Keywords: calcium binding; cytokine; EF hand; heterodimer; homodimer; inflammation
F:2-89/Product: calgranulin A status experimental <MAT>
F:7-41/Domain: calmodulin repeat homology <EF1>
F:46-78/Domain: calmodulin repeat homology <EF2>

alignment_scores:
      Quality: 295.00      Length: 89
      Ratio: 3.734      Gaps: 0
Percent Similarity: 88.764      Percent Identity: 58.427

alignment_block:
US-09-806-382A-1 x I56163 ..

Align seg 1/1 to: I56163 from: 1 to: 89

1   ANGTTGAGCCGAGCTGGAGAAAGCCTTGAACTATCATCGAGCTACCA 50
||| .....|||||.....
1 MetProSeGcluleuGlulysAlaleuSerAsnLeuIleAspValTyrHl 17

51 CAAGTACTCCCTGATAAAGGGGAATTTCATGCCGCTACAGGATGAC 100
|||.....|||||.....
17 sasnYrSerAsnIllegInglYasnHisHisAlaleuTyrlYlsAsnAsp 34

101 TGAAGAATGTCTAGAGACCAGAGTGTCTCAGTAPATCAGAAAAAGGT 150
|||.....
34 helYlsYmetValThrtThrGlucYsProGlnpheValGlnAsnIleasn 50

151 GGAGACGTGTGCTCAAGATGGATATCACACATGATGCAGCCACTTA 200
|||.....
51 IllegluAsnLeupheargIuleuasprIleasnSerAspAsnAlalleas 67

201 CTTCCAGAGATTCCTCATCTGTCGTGATAAAGATGGCGCGAGCCACA 250
|||||.....
67 npheglugluPhelAleuAlameValIlelyValGIyValAlaserHisL 84

251 AAAAAAGCCATGAGAAA 267
|| .....
84 ysAspserHislysglu 89

seq_name: pIr2:B42628

seg_documentation_block:
calcium-binding protein MRP-8 - bovine (fragment)
N:Alternate names: neutrophil cytosolic 7K phosphoprotein; nuclear protein 1
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999
C:Accession: B42628; A22309
R:Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.
Biochemistry 31, 5898-5905, 1992
A>Title: The 23-kDa calmodulin protein, a substrate of protein kinase C, in bovine neutrophils
A:Reference number: A42628; MUID:92304974
A:Accession: B42628
A:Molecule type: protein
A:Residues: 1-41 <DIA>
R:Tang, T.R.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,
submitted to the Protein Sequence Database, July 1992
A:Reference number: A22309
A:Accession: A22309
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9, 'NI', 12-21, 'K', 23-29 <TAN>
C:Superfamily: S-100 protein; calmodulin repeat homologs
C:Keywords: calcium binding; cytosol; EF hand; phosphoprotein

```

```

Alignment_scores:      Quality: 170.00      Length: 41
                       Ratio: 4.595      Gaps: 0
Percent Similarity: 90.244      Percent Identity: 78.049

Alignment_block:
US-09-806-382A-1 x B42628 ..

Align seg 1/1 to B42628 from: 1 to: 41

1 ATGTTGACCGAGCTGGAGAAACCTTGAACTCTATCATCGACGCTTACCA 50
|||||.....|
1 MetLeuThraspleuGlu***AlaIleAspSerLeuIleAspValTyrH 17
51 CAGATGACGCCCTGATAAAGGGAATTCCTACGCGCTCAGAGATGACG 100
|||||.....|
17 StyIYrSerLeu***LysGIYAsnTyrHISAlaValTyr***AspAspL 34
101 TGAGAGAAATTCCTAGACCGAG 123
|||||.....|
34 eulys***LeuIeuGIuThrGlu 41

seq_name: pir2:JC4712

seq_documentation_block:
S-100 calcium-binding protein A12 - human
S:Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; c
ntrophil protein
C:Species: Homo sapiens (man)
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 13-Aug-1999
C:Accession: JC4712; JC4717,JC4891; S56113; S56114
R:Yamamura, T.; Hltoml, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsuka
Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping
A:Reference number: JC4712; MUID:96192053
A:Accession: JC4712
A:Molecule type: mRNA
A:Residues: 1-92 <YAK>
A:Cross-references: DDBJ:D83657; NID:g1502284; PIDN:BAAL2030.1; PID:g1502285
R:Marli, T.; Ertmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequen
A:Reference number: JC4717; MUID:96192069
A:Accession: JC4717
A:Molecule type: protein
A:Residues: 2-92 <MAR>
A:Experimental source: Onchocerca volvulus infecting human tissue
R:Ilb, E.C.; Troxler, H.; Buerisser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hu
Biochem. Biophys. Res. Commun. 225, 146-150, 1996
A:Title: Amino acid sequence determination of human S100 A12 (P6, calgranulin C, CGRP
A:Reference number: JC4891; MUID:96332419
A:Accession: JC4891
A:Molecule type: protein
A:Residues: 2-92 <ILG>
R:Guignard, F.; Meunel, J.; Markert, M.
Biochem. J. 309, 395-401, 1995
A:Title: Identification and characterization of a novel human neutrophil protein rela
A:Reference number: S56113; MUID:95351965
A:Accession: S56113
A:Molecule type: protein
A:Status: preliminary
A:Residues: 'XX',4-14,'X',16-17,'XXXX' <GUII>
A:Experimental source: isoform 6a
A:Accession: S56114
A:Status: preliminary
A:Molecule type: protein
A:Residues: 2-21 <GUI2>
A:Experimental source: isoform 6b
C:Comment: This protein is released by activated neutrophils in the course of inflamm
:Genetics:
:Gene: GDB:S100A12; p6; MRP6; CGRP; CAAF1

```

A:Cross-references: GDB:5218374
 A:Map position: 1q21-1q21
 C:Complex: monomer
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
 F:2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAT>
 F:6-39/Domain: calmodulin repeat homology <EF1>
 F:49-81/Domain: calmodulin repeat homology <EF2>
 F:86-90/Region: zinc binding #status predicted

alignment_scores:
 Quality: 158.00 Length: 96
 Ratio: 2.508 Gaps: 2
 Percent Similarity: 65.625 Percent Identity: 38.542

alignment_block:
 US-09-806-382a-1 x JC4712 ..

Align seg 1/1 to: JC4712 from: 1 to: 92

```

4 TTGACCGAGCTGGAGAAAGCCTTGAACCTGATCATGACGCTACCAAA 53
  ::::::::::::::::::::|::::::::::::::::::|:::
1 MetThrLysLeuGluGlnHisLeuGlnGlyLevalAsnIlePheHisG1 17
54 GTACTCCCTGATTAAGGGGAATTTCCATGCCGTACAGGAGTACCTGA 103
  ::::::::::::::::::::|::::::::::::::::::|:::
17 nlyrSerValArgLysGlyHisPheAspThrLeuSerLysGlyGluLeu 34
104 AGAAATTGCTAGAGACCGAGTGTCCCTCAGTATATCAGG..... 141
  ::::::::::::::::::::|::::::::::::::::::|:::
34 yGlnLeuLeuThrLysGlnLeuAlaAsnThrIleLysAsnIleLysAsp 50
142 AAAAAGGGTGCAGACGCTGTGTTCAAGATGATATCAACACTATGG 191
  ::::::::::::::::::::|::::::::::::::::::|:::
51 LysAlaValIleAspGlnIlePheGlnGlyLeuAspAlaAsnGlnAspG1 67
192 TGCAGTTAACTTCCAGAGAGTCTCTCATTTCTGTGATTAAGATGGCGGTG 241
  ::::::::::::::::::::|::::::::::::::::::|:::
67 uGlnValAspPheGlnGlnPheIleSerLeuVal.....AlaI 80
242 CAGCCCAACAAAAAGCCATGAAGAAAGCCACAAAGAG 279
  ::::::::::::::::::::|::::::::::::::::::|:::
80 LealLeuLysAlaAlaHisThrYHisThrHisLysGln 92

```

seq_name: p1r1:A42628

seq_documentation_block:

calgranulin B - bovine (fragment)
 N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor
 in 2
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997
 C:Accession: B22309; A42628
 R:Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,
 Submitted to the Protein Sequence Database, July 1992
 A:Reference number: A22309
 A:Accession: B22309
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-122 <TAN>
 R:Dianoux, A.C.; Stasia, M.J.; Garlin, J.; Gagnon, J.; Vignais, P.V.
 Biochemistry 31, 5898-5905, 1992
 A:Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophil
 A:Reference number: A42628; MUID:92304974
 A:Accession: A42628
 A:Molecule type: protein
 A:Residues: 4-32, 'F', '34-56 <DIA>
 C:Complex: heterodimer and higher complexes with calgranulin A
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phos
 F:6-40/Domain: calmodulin repeat homology <EF1>
 F:50-82/Domain: calmodulin repeat homology <EF2>

alignment_scores:
 Quality: 154.50 Length: 91
 Ratio: 2.239 Gaps: 1
 Percent Similarity: 75.824 Percent Identity: 27.473

alignment_block:
 US-09-806-382a-1 x A42628 ..

Align seg 1/1 to: A42628 from: 1 to: 122

```

4 TTGACCGAGCTGGAGAAAGCCTTGAACCTGATCATGACGCTACCAAA 53
  ::::::::::::::::::::|::::::::::::::::::|:::
1 MetSerGlnMetGlnSerSerIleGlnThrIleIleAsnIlePheHisG1 17
54 GTACTCCCTGATTAAGGGGAATTTCCATGCCGTACAGGAGTACCTGA 103
  ::::::::::::::::::::|::::::::::::::::::|:::
17 nlyrSerValArgLysGlyHisPheAspThrLeuSerLysGlyGluLeu 34
104 AGAAATTGCTAGAGACCGAGTGTCCCTCAGTATATCAGGAAAAAG..... 147
  ::::::::::::::::::::|::::::::::::::::::|:::
34 yGlnLeuValAlaGlnLysGlnLeuProAsnPheLeuLysGlnLysLys 50
51 AsnGlnAlaAlaIleAsnGlnIleMetGlnAspLeuAspThrAsnValas 67
148 .....GTGCAGACGCTGTGTTCAAGATGATATCAACACTGA 188
  ::::::::::::::::::::|::::::::::::::::::|:::
189 TGTGCACTTAACCTTCCAGAGAGTCTCTCATTTCTGTGATTAAGATGGCG 238
  ::::::::::::::::::::|::::::::::::::::::|:::
67 pLysGlnLeuSerPheGlnGlnPheIleMetGlnAspLeuValAlaArgLeuThr 84
239 TGCAGCCCAACAAAAAGCCAT 261
  ::::::::::::::::::::|::::::::::::::::::|:::
84 AlaIleSerHisGlnGlnMetHis 91

```

seq_name: p1r2:S24146

seq_documentation_block:

S-100 protein P - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S24146; PS0340
 R:Becker, T.; Gerke, V.; Kube, E.; Weber, K.
 Eur. J. Biochem. 207, 541-547, 1992
 A:Title: S100P, a novel Ca(2+)-binding protein from human placenta. cDNA cloning, rec
 A:Reference number: S24146; MUID:92339442
 A:Accession: S24146
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-95 <BEC>
 A:Cross-references: EMBL:X65614; NID:g36177; PIDN:CAA46566.1; PID:g36178
 R:Emoto, Y.; Kobayashi, R.; Akatsuka, H.; Hidaka, H.
 Biochem. Biophys. Res. Commun. 182, 1246-1253, 1992
 A:Title: Purification and characterization of a new member of the S-100 protein fam1
 A:Reference number: PS0340; MUID:92171935
 A:Accession: PS0340
 A:Molecule type: protein
 A:Residues: 1-31, 'F', '33-84, 'X', '86-91 <EMO>
 A:Experimental source: placenta
 C:Genetics:
 A:Gene: GDB:S100P
 A:Cross-references: GDB:134405; OMIM:600614
 A:Map position: 4p16-4p16
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand; placenta
 F:6-40/Domain: calmodulin repeat homology <EF1>
 F:49-81/Domain: calmodulin repeat homology <EF2>

alignment_scores:
 Quality: 154.00 Length: 87
 Ratio: 2.525 Gaps: 1

US-09-806-382a-1 x BCHUIB ..

Align seg 1/1 to: BCHUIB from: 1 to: 92

```

4 TTGACCGAGCTGGAGAAAGCCTTGAACCTATCATCGACGCTTACCACAA 53
  :::::::::::::::::::::
1 MetSerGluLeuGluValAlaMetValAlaLeuIleAspValPheHisG1 17
54 GTCATCCCGCATAAAGGGAATTTCCATGCCCTACACAGGATGACCTGA 103
  :::::::::::::::::::::
17 nlyrSerGlyArgGluGlyAspLysHisLysLysLysSerGluLeuL 34
104 AGAAATTGCTAGAGACCGAGCTGCTCATGATATAC.....AGG 141
  :::::::::::::::::::::
34 ysglLeuIleAsnAsnGluLeuSerHisPheLeuGluGluIleLysGlu 50
142 AAAAAGGTGACAGACGCTGTGTTCAAGAAGTTGATATCAACACATGATG 191
  :::::::::::::::::::::
51 GInGluValAlaIAspLysValMetGluThrLeuAspAsnAspGlyAspG1 67
192 TGCAGTTAACTCCAGAGACTTCCTCATCTGTGTGTTAAAGATGGCGCTGG 241
  :::::::::::::::::::::
67 yglucyAspPheGlnGluPheMetAlaPheValAlaMetValThrThra 84
242 CAGCCACACAA 252
  :::::::::::::::::::::
84 lacySHisGlu 87

```

seq_name: pir2:A48015

seq_documentation_block:

S-100 protein beta chain - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Nov-1999
 C:Accession: A48015
 R:Jiang, H.; Shah, S.; Hilt, D.C.
 J. Biol. Chem. 268, 20502-20511, 1993
 A:Title: Organization, sequence, and expression of the murine S100beta gene. Transcript
 A:Reference number: A48015; MUID:93388628
 A:Accession: A48015
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-92 <JIA>
 A:Cross-references: GB:I22144; NID:g404768; PIDN:AAA03075.1; PID:g404769
 C:Genetics:
 A:Introns: 46/3
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: acetylated amino end; calcium binding; EF hand
 F:2-92/Product: S-100 protein beta chain #status predicted <MAT>
 F:6-40/Domain: calmodulin repeat homology <EF1>
 F:49-81/Domain: calmodulin repeat homology <EF2>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
 F:20,22,24,27,32/Binding site: calcium (Gly, Glu, Asp, Lys, Glu) #status predicted
 F:62,64,66,68,70,73/Binding site: calcium (Asp, Asp, Glu, Asp, Glu) #status predict

alignment_scores:

Quality:	Length:
139.00	87
Ratio: 2.206	Gaps: 1
Percent Similarity: 72.414	Percent Identity: 33.333

alignment_block:

US-09-806-382a-1 x A48015 ..

Align seg 1/1 to: A48015 from: 1 to: 92

```

4 TTGACCGAGCTGGAGAAAGCCTTGAACCTATCATCGACGCTTACCACAA 53
  :::::::::::::::::::::
1 MetSerGluLeuGluValAlaMetValAlaLeuIleAspValPheHisG1 17
54 GTCATCCCGCATAAAGGGAATTTCCATGCCCTACACAGGATGACCTGA 103
  :::::::::::::::::::::
17 nlyrSerGlyArgGluGlyAspLysHisLysLysLysSerGluLeuL 34

```

```

104 AGAAATTGCTAGAGACCGAGCTGCTCATGATATAC.....AGG 141
  :::::::::::::::::::::
34 ysglLeuIleAsnAsnGluLeuSerHisPheLeuGluGluIleLysGlu 50
142 AAAAAGGTGACAGACGCTGTGTTCAAGAAGTTGATATCAACACATGATG 191
  :::::::::::::::::::::
51 GInGluValAlaIAspLysValMetGluThrLeuAspLysValAspG1 67
192 TGCAGTTAACTCCAGAGACTTCCTCATCTGTGTGTTAAAGATGGCGCTGG 241
  :::::::::::::::::::::
67 yglucyAspPheGlnGluPheMetAlaPheValAlaMetValThrThra 84
242 CAGCCACACAA 252
  :::::::::::::::::::::
84 lacySHisGlu 87

```

seq_name: pir2:A26557

seq_documentation_block:

S-100 protein beta chain - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Mar-1988 #sequence_revision 04-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A60046; S07357; A26557
 R:Maeda, T.; Usui, H.; Araki, K.; Kuwano, R.; Takahashi, Y.; Suzuki, Y.
 Brain Res. Mol. Brain Res. 10, 193-202, 1991
 A:Title: Structure and expression of rat S-100 beta subunit gene.
 A:Reference number: A60046; MUID:91359841
 A:Accession: A60046
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-92 <MAE>
 A:Cross-references: GB:S53527
 R:Kuwano, R.; Usui, H.; Maeda, T.; Fukui, T.; Yamanari, N.; Ohtsuka, E.; Ikehara, M.;
 Nucleic Acids Res. 12, 7455-7465, 1984
 A:Title: Molecular cloning and the complete nucleotide sequence of cDNA to mRNA for S
 A:Reference number: S07357; MUID:85037924
 A:Accession: S07357
 A:Molecule type: mRNA
 A:Residues: 1-92 <KUM>
 A:Cross-references: EMBL:X01090; NID:957174; PIDN:CAA25567.1; PID:957175
 R:Dunn, R.; Landry, C.; O'Hanlon, D.; Dunn, J.; Allore, R.; Brown, I.; Marks, A.
 J. Biol. Chem. 262, 3562-3566, 1987
 A:Title: Reduction in S100 protein Beta-subunit mRNA in C6 rat glioma cells following
 A:Reference number: A26557; MUID:87137648
 A:Accession: A26557
 A:Molecule type: mRNA
 A:Residues: 6-92 <DUN>
 A:Cross-references: GB:M15705
 C:Comment: S-100 protein occurs as alpha-beta heterodimers, alpha-alpha heterodimers,
 C:Genetics:
 A:Introns: 46/3
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: brain; calcium binding; dimer; EF hand; zinc
 F:2-92/Product: S-100 protein beta chain #status predicted <MAT>
 F:6-40/Domain: calmodulin repeat homology <EF1>

alignment_scores:

Quality:	Length:
138.00	87
Ratio: 2.190	Gaps: 1
Percent Similarity: 72.414	Percent Identity: 33.333

alignment_block:

US-09-806-382a-1 x A26557 ..

Align seg 1/1 to: A26557 from: 1 to: 92

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4 TTGACCGAGCTGGAGAAAGCCTTGAACCTATCATCGACGCTTACCACAA 53
  :::::::::::::::::::::
1 MetSerGluLeuGluValAlaMetValAlaLeuIleAspValPheHisG1 17
54 GTCATCCCGCATAAAGGGAATTTCCATGCCCTACACAGGATGACCTGA 103

```

```

|||||  :::::  |||  ::  ::::::::::|||
17 nfyserglaryarglgllyasplyshlslyseuylslyssergluleu 34
104 AGAAATGCTAGAGACCGAGTCTCTCACTATATC.....AGG 141
34 ysluleuileasnsngluleuserhlsphleucluleylsglu 50
142 AAAAAGGCGCAGCGTCTGGTTCAAGAGTGGATATCAACACGTGATG 191
51 glngluvalvalasplysvalmetgluthtlreusapgluaspoly 67
192 TGCACTTAACCTTCAGAGATTCCTCATTTCTGGTGAATMAAGATGGCGTGG 241
67 yglucysasphneglngluhphemetaphavalsermetvalthrttha 84
242 CAGCCCAAAA 252
84 lacyshlsglu 87

seq_name: p1r1:BCBOIB

seq_documentation_block:
S-100 protein beta chain - bovine
N:Alternate names: neurocalcin delta-binding protein s100-beta
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-May-1979 #sequence_revision 14-Nov-1983 #text_change 24-Nov-1999
C:Accession: A91254; B91110; A90075; S54348; A03077
R:Isoe: T.; Okuyama, T.
Eur. J. Biochem. 89, 379-388, 1978
A:Title: The amino-acid sequence of S-100 protein (PAP-I-b protein) and its relation to
A:Reference number: A91254; MUID:79045265
A:Accession: A91254
A:Molecule type: protein
A:Residues: 'ESEL', 5-91 <ISO>
A:Experimental source: brain
A:Note: This sequence has since been revised in reference A91110
R:Isoe: T.; Okuyama, T.
Eur. J. Biochem. 116, 79-86, 1981
A:Title: The amino-acid sequence of the alpha subunit in bovine brain S-100 a protein.
A:Reference number: A91110; MUID:81236562
A:Accession: B91110
A:Molecule type: protein
A:Residues: 1-91 <IS2>
R:Baudier, J.; Gerard, D.
Biochemistry 22, 3360-3369, 1983
A:Title: Ions binding to S100 proteins: structural changes induced by calcium and zinc C
A:Reference number: A90471; MUID:84000339
A:Contents: annotation; metal ion-binding properties
R:Marshak, D.R.; Umekawa, H.; Waterson, D.M.; Hidaka, H.
Arch. Biochem. Biophys. 240, 777-780, 1985
A:Title: Structural characterization of the calcium binding protein S100 from adipose ti
A:Reference number: A90075; MUID:85278169
A:Accession: A90075
A:Molecule type: protein
A:Residues: 1-91 <MAR>
A:Experimental source: adipose tissue
R:Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A:Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia
A:Reference number: S54343; MUID:95194333
A:Accession: S54348
A:Molecule type: protein
A:Residues: 56-61, 'N', 63-79, 'V' <OKA>
C:Comment: The S-100 protein is composed of two related polypeptide chains, alpha and be
brain proteins. S-100 is also found in a variety of other tissues.
C:Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc ve
es with different affinities exist for both ions on each monomer. Physiological concentr
cium-binding sites.
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; brain; calcium binding; EF hand; zinc
F:48-80/Domain: calmodulin repeat homology <EF2>
F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental

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```

F:18,21,23,26,31/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
F:61,63,65,67,72/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted

alignment_scores:
Quality: 137.00 Length: 86
Ratio: 2.210 Gaps: 1
Percent Similarity: 72.093 Percent Identity: 33.721

alignment_block:
US-09-806-382a-1 x BCBOIB ..

Align seg 1/1 to: BCBOIB from: 1 to: 91

7 ACCGACGTGAGAGAGCGTGAACCTATCATCATGACGTACACCAAGTA 56
:|||||  :::::  |||  ::  ::::::::::|||
1 sergluleuileuysalvalalaleuileasplyalphenlsinty 17
17 rserglaryarglgllyasplyshlslyseuylslyssergluleuylsg 34
57 CTCCTGATMAAGGGGAATTTCCATGCCGTCTACAGAGATGACCTGAAGA 106
|||||  :::::  |||  ::  ::::::::::|||
34 luleuileasnsngluleuserhlsphleucluleylsglulin 50
107 AATGCTAGAGACCGAGTCTCTCACTATATC.....AGGAAA 144
:|||||  :::::  |||  ::  ::::::::::|||
34 luleuileasnsngluleuserhlsphleucluleylsglulin 50
145 AAGCGTCAGAGCGTCTGGTTCAAGAGTGGATATCAACACGTGATGTCG 194
:|||||  :::::  |||  ::  ::::::::::|||
51 glulvalvalasplysvalmetgluthtlreusaspseraspolygl 67
195 AGTTAATTCAGAGATTCCTCATTTCTGGTGAATMAAGATGGCGTGCAG 244
:|||||  :::::  |||  ::  ::::::::::|||
67 ucysasphneglngluhphemetaphavalalawetletthrtthlalc 84
245 CCGACAAA 252
84 yshlsglu 86

seq_name: p1r1:S35985

seq_documentation_block:
S-100 protein alpha chain - weatherfish
C:Species: Misgurnus fossilis (weatherfish)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S35985
R:Rivanekov, V.V.; Gerke, V.; Minhn, A.A.; Plesmann, U.; Weber, K.
Mech. Dev. 42, 151-156, 1993
A:Title: Transduction of Ca(2+) signals upon fertilization of eggs; Identification of
A:Reference number: S35985; MUID:94031845
A:Accession: S35985
A:Molecule type: protein
A:Residues: 1-95 <IVA>
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:49-81/Domain: calmodulin repeat homology <EF2>

alignment_scores:
Quality: 134.00 Length: 92
Ratio: 2.271 Gaps: 2
Percent Similarity: 64.130 Percent Identity: 34.783

alignment_block:
US-09-806-382a-1 x S35985 ..

Align seg 1/1 to: S35985 from: 1 to: 95

4 TTAGCGACGTGAGAGAGCGTGAACCTATCATCATGACGTACACCAAA 53
:|||||  :::::  |||  ::  ::::::::::|||
1 valsergluleuileuysalvalalaleuileasplyalphenlsinty 17
54 GTACTCCCTGATMAAGGGGAATTTCCATGCCGTCTACAGAGATGACCTGA 103
|||||  :::::  |||  ::  ::::::::::|||

```

17 rTyrSerSerLysGluGlyAspLysTyrLysLeuSerLysAlaGluLeuL 34
104 AGAATGCTAGAGACCGAGTGT..... 126
||::||| |||
34 ySerLeuLeuGlnGlyIleuAsnAspPheLeuSerAlaSerLysAsp 50
127 CCTCAGTATATCAGGAAAAGGTCAGACCTGTCTGTCAAGAGTTGGA 176
|||::: ||| |||
51 ProMetValValGluLysIleMetSerAsp.....LeuAs 62
177 TATCAACACTGATGGTGCAGTTAACTCCAGAGATTCTCATTTGTGTA 226
| ||| ||| |||::: ||| |||::: ||| |||
62 pGluAsnGlnAspGlyIleValAspPheGlnGluPheValValLeuValA 79
227 TAAAGATGGGCGTGCAGCCACACAAA 252
:: |||::: |||
79 laAlaLeuThrValAlaCysAsnGlu 87

OM of: US-09-806-382a-1 to: SwissProt_40.* out_format : pfs

Date: Sep 9, 2002 3:22 PM

About: Results were produced by the Gencore software, version 4.5,
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Command line parameters:

-MODEL=frame+ncp.model -DEV=xlp
-O=/cgn2_1/USPRO.spool/US09806382/rnat_09092002.143849_15565/app_query.fasta.1.752
-DB=SwissProt_40 -OFORMAT=FASTA -SUFFIX=rs -GAPOP=12.000
-GAPEXT=4.000 -MISMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=0.000 -DELEXT=7.000 -START=1 -MATRIX=blonsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=PCT
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OFFFMT=PFS
-NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09806382.#CGN1.1.62 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-806-382a-1

Query length: 282

Database: SwissProt_40.*

Database sequences: 105224

Database length: 38719550

Search time (sec): 32.310000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SwissProt_40:S108_HUMAN + 485.00	1000.28	5.5e-48	93	P05109	homo sapiens (human).
SwissProt_40:S108_RAT + 320.00	659.13	5.8e-29	88	P50115	rattus norvegicus (rat).
SwissProt_40:S108_MOUSE + 293.00	603.23	7.6e-26	88	P27005	mus musculus (mouse).
SwissProt_40:S108_BOVIN + 170.00	355.03	1.1e-11	41	P28782	bos taurus (bovine).
SwissProt_40:M126_CHICK + 169.50	344.94	1.4e-11	119	P28318	gallus gallus (chick).
SwissProt_40:S112_BOVIN + 158.00	323.45	2.8e-10	91	P79105	bos taurus (bovine).
SwissProt_40:S109_BOVIN + 156.50	317.86	4.3e-10	122	P28783	bos taurus (bovine).
SwissProt_40:S112_HUMAN + 156.00	319.31	4.8e-10	91	P80511	homo sapiens (human).
SwissProt_40:S10E_HUMAN + 154.00	314.80	8.1e-10	95	P25815	homo sapiens (human).
SwissProt_40:S112_PIG + 151.00	308.95	1.8e-09	91	P80310	sus scrofa (pig).
SwissProt_40:S10A_RAT + 148.00	302.56	4.0e-09	93	P35467	rattus norvegicus (rat).
SwissProt_40:S10A_BOVIN + 146.00	298.42	6.8e-09	93	P26630	bos taurus (bovine).
SwissProt_40:S10A_HUMAN + 144.00	294.28	1.2e-08	93	P23297	homo sapiens (human).
SwissProt_40:S10A_MOUSE + 139.00	283.93	4.4e-08	93	P26565	mus musculus (mouse).
SwissProt_40:S10B_BOVIN + 137.00	279.97	7.4e-08	91	P02638	bos taurus (bovine).
SwissProt_40:S10B_HUMAN + 137.00	279.97	7.4e-08	91	P04271	homo sapiens (human).
SwissProt_40:S10B_MOUSE + 137.00	279.97	7.4e-08	91	P05014	mus musculus (mouse).
SwissProt_40:S10B_RAT + 136.00	277.90	9.7e-08	91	P04631	rattus norvegicus (rat).
SwissProt_40:S109_HUMAN + 133.50	270.82	1.9e-07	114	P06702	homo sapiens (human).
SwissProt_40:S109_MOUSE + 131.50	266.83	3.2e-07	112	P31725	mus musculus (mouse).
SwissProt_40:S111_MOUSE + 131.00	266.92	3.7e-07	98	P50143	mus musculus (mouse).
SwissProt_40:S109_RAT + 130.50	264.76	4.2e-07	112	P50116	rattus norvegicus (rat).
SwissProt_40:S107_BOVIN + 127.50	259.42	9.3e-07	101	P02805	bos taurus (bovine).
SwissProt_40:S112_RABIT + 127.00	250.25	1.0e-06	81	P07791	oryctolagus cuniculus.
SwissProt_40:S104_HUMAN + 126.00	256.31	1.4e-06	101	P26447	homo sapiens (human).
SwissProt_40:S104_BOVIN + 125.00	252.17	2.4e-06	100	P35466	bos taurus (bovine).
SwissProt_40:S104_MOUSE + 124.00	248.73	4.0e-06	93	P07991	mus musculus (mouse).
SwissProt_40:S105_HUMAN + 122.00	247.95	4.0e-06	102	P24480	oryctolagus cuniculus.
SwissProt_40:S111_RABIT + 121.50	245.68	4.6e-06	118	P50117	oryctolagus cuniculus.
SwissProt_40:S104_RAT + 121.00	245.96	5.2e-06	101	P05942	rattus norvegicus (rat).
SwissProt_40:S111_CHICK + 121.00	245.96	5.2e-06	101	P24479	gallus gallus (chick).
SwissProt_40:S105_HUMAN + 120.50	244.20	6.0e-06	110	P33763	homo sapiens (human).
SwissProt_40:S10D_BOVIN + 119.50	244.04	7.6e-06	78	P02633	bos taurus (bovine).
SwissProt_40:S10D_HUMAN + 118.50	241.13	1.0e-05	97	P02632	homo sapiens (human).
SwissProt_40:S10D_PIG + 115.50	236.76	2.2e-05	78	P02632	sus scrofa (pig).
SwissProt_40:S106_RABIT + 113.00	230.37	4.3e-05	90	P30801	oryctolagus cuniculus.
SwissProt_40:S101_ICPUP + 112.50	228.12	4.9e-05	72	P29377	homo sapiens (human).
SwissProt_40:S101_ICPUP + 112.00	228.12	5.7e-05	98	P09106	ictaluricus punctatus (c).
SwissProt_40:S102_BOVIN + 112.00	227.67	5.7e-05	97	P10462	bos taurus (bovine).

seq_name: SwissProt_40:S108_HUMAN	seq_documentation_block:	ID	S108_HUMAN	STANDARD:	PRT:	93 AA.
SwissProt_40:S111_PIG + 112.00	227.50	5.7e-05	99	P31950	sus scrofa (pig).	cal
SwissProt_40:S111_HUMAN + 111.00	224.93	7.5e-05	105	P31949	homo sapiens (human).	cal
SwissProt_40:S110_CHICK + 110.50	224.65	8.5e-05	96	P27003	gallus gallus (chick).	cal
SwissProt_40:S106_HUMAN + 110.00	224.16	9.6e-05	90	P06703	homo sapiens (human).	cal
SwissProt_40:TRH_RABIT + 110.00	200.92	0.0001	1407	P37709	oryctolagus cuniculus.	cal
seq_name: SwissProt_40:S108_HUMAN	seq_documentation_block:	ID	S108_HUMAN	STANDARD:	PRT:	93 AA.
AC	P05109:					
DT	13-AUG-1987 (Rel. 05, Created)					
DT	01-JAN-1988 (Rel. 06, Last sequence update)					
DT	01-MAR-2002 (Rel. 41, Last annotation update)					
DE	Calgranulin A (Migration inhibitory factor-related protein 8) (MRP-8)					
DE	(Cystic fibrosis antigen) (CFAG) (P8) (Leukocyte L1 complex light chain) (S100 calcium-binding protein A8).					
GN	S100A8 OR MRP8 OR CACA.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=88039099; PubMed=3313057;					
RA	Odink K., Cerletti N., Bruggen J., Clerc R.G., Tarsay L., Zwaldo G.,					
RA	Gerhards G., Schlegel R., Sorg C.;					
RT	"Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis."					
RL	Nature 330:80-82(1987).					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=88302148; PubMed=3405210;					
RA	Lagasse E., Clerc R.G.;					
RT	"Cloning and expression of two human genes encoding calcium-binding proteins that are regulated during myeloid differentiation."					
RL	Mol. Cell. Biol. 8:2402-2410(1988).					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=87173041; PubMed=3561500;					
RA	Dorin J.R., Novak M., Hill R.E., Brock D.J.H., Secher D.S.,					
RA	van Heyningen V.;					
RT	"A clue to the basic defect in cystic fibrosis from cloning the CF antigen gene."					
RL	Nature 326:614-617(1987).					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=91248411; PubMed=2039599;					
RA	Schaefer T., Sachse G.E., Gassen H.G.;					
RT	"The calcium-binding protein MRP-8 is produced by human pulmonary tumor cells."					
RL	Biol. Chem. Hoppe-Seyler 372:1-4(1991).					
RP	SEQUENCE OF 38-47 AND 50-56.					
RC	TISSUE=Keratinocytes;					
RX	MEDLINE=93162043; PubMed=1286667;					
RA	Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,					
RT	"Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes."					
RL	Electrophoresis 13:960-969(1992).					
RP	SEQUENCE OF 1-19; 24-35 AND 63-89.					
RX	MEDLINE=96192069; PubMed=8619876;					
RA	Marti T., Ertmann K.D., Gallin M.Y.;					
RT	"Host-parasite interaction in human onchocerciasis: identification and sequence analysis of a novel human calgranulin A."					
RL	Biochem. Biophys. Res. Commun. 221:454-458(1996).					
RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).					
RX	MEDLINE=20235649; PubMed=10771424;					
RA	Ishikawa K., Nakagawa A., Tanaka I., Suzuki M., Nishihira J.;					
RT	"The structure of human MRP8, a member of the S100 calcium-binding					

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RT protein family, by MAD phasing at 1.9 A resolution.";
RL Acta Crystallogr. D 56:559-566(2000).
CC -1- FUNCTION: EXPRESSED BY MACROPHAGES IN CHRONIC INFLAMMATIONS. ALSO
CC EXPRESSED IN EPITHELIAL CELLS CONSTITUTIVELY OR INDUCED DURING
CC DERMATOSIS. MAY INTERACT WITH COMPONENTS OF THE INTERMEDIATE
CC FILAMENTS IN MONOCYTES AND EPITHELIAL CELLS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- MISCELLANEOUS: BINDS TWO CALCIUM IONS PER MOLECULE WITH AN
CC AFFINITY SIMILAR TO THAT OF THE S-100 PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y00378; CA68390.1; -
DR EMBL; X06234; CA29580.1; -
DR EMBL; M21005; AA36327.1; -
DR EMBL; A12027; CA01001.1; -
DR PIR; A29764; BCHUCF.
DR PIR; A31848; A31848.
DR PIR; S13454; S13454.
DR PDB; 1MR8; 17-MAT-00.
DR Aarhus/Ghent-2DPAGE; 1003; IEF.
DR PMMA-2DPAGE; P05109; -
DR MIM; 123885; -
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_Cabp.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
DR Macrophage; Calcium-binding; 3D-structure.
FT CA_BIND 20 33 EF-HAND 1 (LOW AFFINITY).
FT CA_BIND 59 70 EF-HAND 2 (HIGH AFFINITY).
FT CONFLICT 79 93 GVAHKKSHESHKE -> AMOPTKAMKKATKSS
FT SEQUENCE 93 AA; 10834 MW; 78F589140B9CE16 CRC64;
SQ
alignment_scores:
Quality: 485.00 Length: 93
Ratio: 5.215 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-806-382A-1 x S108_HUMAN ..
Align seg 1/1 to: S108_HUMAN from: 1 to: 93
1 ATGTGACGAGCTGGAGAAAGCCCTGAACCTATCATGACGCTACCA 50
|||||
1 MetLeuThGlueuGlulysAlaLeuAAsenTlleleSpAllyrHl 17
51 CAAGTACTCCCTGATAAAGGGAATTCATGCGCTACAGGATGACC 100
|||||
17 slYsYrSerLeuIleLysGlYasnPhenIslaValIYrArGAspAspL 34
101 TGAAGAAATTCGTAGAGACCGAGTGCCTCAGTATATCAGGAAAAAGGT 150
|||||
34 euLysYsLeuLeuGlutHnGlucYsProGlnTyrIleAqLysLysGly 50
151 GCAGAGCTGTGTTCAAGAGTGTGATATCAACACTGATGTCACATTA 200
|||||
51 AlaAspValItrpHelysgLuleuAAspIleAsnThrAspGlyAlaValas 67
202 CTTTCAGAGATTCCTCATTCGTGTTGATTAAGATGGCGTGCGACCCACA 250
|||||

```

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67 nPhenGlnuPhenLeuIleuValIleLysMetGlyValAlaAlaHsl 84
251 AAAAAAGCCATGAAGAAAGCCACAAAGAG 279
|||||
84 yslYsSerHlsGluGluSerHlsLysGlu 93
seq_name: SwissProt_40:S108_RAT
seq_documentation_block:
ID S108_RAT STANDARD; PRT; 88 AA.
AC P50115;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calgranulin A (Migration inhibitory factor-related protein 8) (MRP-8)
DE (P8).
GN S100A8 OR MRP8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEWIS/N; TISSUE=peritoneal cavity;
RX MEDLINE=93343942; PubMed=8343166;
RA Imanishi T., Uchida I., Wahl S.M., McCartney-Francis N.;
RT "Expression and cloning of migration inhibitory factor-related
RT protein (MRP) 8 and MRP14 in arthritis-susceptible rats.";
RL Biochem. Biophys. Res. Commun. 194:819-825(1993).
RN [2]
RP SEQUENCE, AND ACETYLATION.
RC TISSUE=Spleen.
RX MEDLINE=98249881; PubMed=9570842;
RA Raftery M.J., Geeczy C.L.;
RT "Identification of posttranslational modifications and cDNA sequencing
RT errors in the rat S100 proteins MRP8 and 14 using electrospray
RT ionization mass spectrometry.";
RL Anal. Biochem. 258:285-292(1998).
CC -1- FUNCTION: HAS MAXIMAL CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. MAY
CC PLAY AN IMPORTANT ROLE IN CELLULAR IMMUNE REACTIONS.
CC -1- SUBUNIT: HOMODIMER AND/OR HETERODIMER.
CC -1- MASS SPECTROMETRY: MW=10149; MW_ERR=2; METHOD=Electrospray.
CC -1- MISCELLANEOUS: BINDS TWO CALCIUM IONS PER MOLECULE WITH AN
CC AFFINITY SIMILAR TO THAT OF THE S-100 PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L18891; AAA41637.1; -
DR HSSP; P04631; IBAC.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_Cabp.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR SMART; SM00054; EFh; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
DR Calcium-binding; Chemotaxis; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT CA_BIND 19 32 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 58 69 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
FT CONFLICT 72 72 V -> A (IN REF. 1).
SQ SEQUENCE 88 AA; 10107 MW; 235CE67BA9602D1E CRC64;

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alignment_scores:

Quality: 320.00 Length: 87
Ratio: 3.951 Gaps: 0
Percent Similarity: 93.103 Percent Identity: 63.218

alignment_block:

US-09-806-382a-1 x S108_RAT ..

Align seg 1/1 to: S108_RAT from: 1 to: 88

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7 ACCGAGCTGGAGAAAGCCTTGAACCTATATCACTGACGCTTACCAAGTA 56
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
2 ThrGluLeuGluLysAlaLeuSerValIleGluValIleTyrHisAsnTyr 18
57 CTCCTGATTAAGGGAATTTCCATCCGCTGACAGGATGACCTGAGA 106
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
18 rSerGlyIleLysGlyAsnHisAlaLeuIleTyrArgAspSprPheArgL 35
107 AATTGCTAGAGACCGAGTGTCTCTCAGTATATCAGGAAAGGCTGACAG 156
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
35 yMetValIleThrThrGluLysProGlnPheValGlnAsnLysAsnThrGlu 51
157 GTCGTGCTCAAGAGCTGTGATATCAACACGTAGTGCAGTAACTTCCA 206
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
52 SerLeuPheLysGluLeuAspValAlaSerAspAsnAlaIleAsnPhcgl 68
207 GGAGTTCCTCATCTGCTGATTAAGATGGCGGTGACCCCAAAAAA 256
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
68 uGluPheLeuValLeuValIleArgValGlyValAlaAlaHisLysAspS 85
257 GCCATGAAGAA 267
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
85 eRHsLysGlu 88
seq_name: SwissProt_40:S108_MOUSE
seq_documentation_block:
ID S108_MOUSE STANDARD; PRT; 88 AA.
AC P27005; P31724;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Calgranulin A (Migration inhibitory factor-related protein 8) (MRP-8)
DE (P8) (Leukocyte L1 complex light chain) (Chemotactic cytokine CP-10)
DE (PRO-inflammatory S100 cytokine).
GN S100A8 OR CAGA OR MRP8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=92223366; PubMed=1373330;
RA Lagasse E., Weissman I.L.;
RT "Mouse MRP8 and MRP14, two intracellular calcium-binding proteins
RT associated with the development of the myeloid lineage.";
RL Blood 79:1907-1915(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93203618; PubMed=8454868;
RA Lackmann M., Rajasekariah P., Iismaa S.E., Jones G., Cornish C.J.,
RA Hu S., Simpson R.J., Moritz R.L., Geczy C.L.;
RT "Identification of a chemotactic domain of the pro-inflammatory S100
RT protein CP-10.";
RL J. Immunol. 150:2981-2991(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Liver;
RX MEDLINE=96190772; PubMed=8611640;
RA Nacken W.K.F., Manitz M.P., Sorg C.;
RT "Molecular characterisation of the genomic locus of the mouse MRP8
RT gene.";
```

RL Biochim. Biophys. Acta 1315:1-5(1996).

RN [4]

RP SEQUENCE OF 1-76.

RC TISSUE=Spleen;

RX MEDLINE=92218405; PubMed=1559987;

RA Lackmann M., Cornish C.J., Simpson R.J., Moritz R.L., Geczy C.L.;

RT "Purification and structural analysis of a murine chemotactic

cytokine (CP-10) with sequence homology to S100 proteins.";

RL J. Biol. Chem. 267:7499-7504(1992).

CC -1- FUNCTION: HAS MAXIMAL CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. MAY

PLAY AN IMPORTANT ROLE IN CELLULAR IMMUNE REACTIONS.

CC -1- SUBUNIT: HOMODIMER AND/OR HETERODIMER.

CC -1- MISCELLANEOUS: BINDS TWO CALCIUM IONS PER MOLECULE WITH AN

AFFINITY SIMILAR TO THAT OF THE S-100 PROTEINS (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY

-1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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CC or send an email to license@isb.slb.ch).

CC -----

DR EMBL; M83218; AAB07229.1; -;

DR EMBL; S57123; AAB25840.1; -;

DR EMBL; X87966; CAA61204.1; -;

DR PIR; A42488; A42488.

DR HSSP; P04631; 1BAC.

DR MGD; MGI:86244; S100a8.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001751; S100_Cabp.

DR Pfam; PF00036; efhand; 1.

DR Pfam; PF01023; S_100; 1.

DR PROSITE; PS00018; EF_HAND; 1.

DR PROSITE; PS00303; S100_CABP; 1.

KW Calcium-binding; Chemotaxis.

FT INIT_MET 0 0

FT CA_BIND 19 32 EF_HAND 1 (LOW AFFINITY) (POTENTIAL).

FT CA_BIND 58 69 EF_HAND 2 (HIGH AFFINITY) (POTENTIAL).

FT CONFLICT 56 56 E -> D (IN REF. 3).

SO SEQUENCE 88 AA; 10163 MW; 9B32BDE53CFE728 CRC64;

alignment_scores:

Quality: 293.00 Length: 87
Ratio: 3.756 Gaps: 0
Percent Similarity: 89.655 Percent Identity: 58.621

alignment_block:

US-09-806-382a-1 x S108_MOUSE ..

Align seg 1/1 to: S108_MOUSE from: 1 to: 88

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7 ACCGAGCTGGAGAAAGCCTTGAACCTATATCACTGACGCTTACCAAGTA 56
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
2 SerGluLeuGluLysAlaLeuSerValIleGluValIleTyrHisAsnTyr 18
57 CTCCTGATTAAGGGAATTTCCATCCGCTGACAGGATGACCTGAGA 106
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
18 rSerAsnIleGlnGlyAsnHisAlaLeuIleTyrLysAsnSprPheArgL 35
107 AATTGCTAGAGACCGAGTGTCTCAGTATATCAGGAAAGGCTGACAG 156
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
35 yMetValIleThrThrGluLysProGlnPheValGlnAsnLysAsnThrGlu 51
157 GTCGTGCTCAAGAGCTGTGATATCAACACGTAGTGCAGTAACTTCCA 206
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
52 AsnLeuPheArgLysGluLeuAspIleAsnSerAspAsnAlaIleAsnPhcgl 68
207 GGAGTTCCTCATCTGCTGATTAAGATGGCGGTGACCCCAAAAAA 256
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
```

68 uc1upheleuallamelvalilleysvaliglyvalalaserhislysasps 85
 257 GCCATGAAGAA 267
 |||||
 85 erhislysclu 88

seq_name: SwissProt_40:S108_BOVIN

seq_documentation_block:
 ID S108_BOVIN STANDARD: PRT: 41 AA.
 AC P28782:
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calgranulin A (Neutrophil cytosolic 7 kDa protein) (P7) (BEE11)
 DE (Fragment).
 GN S100A8.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Neutrophils;
 RX MEDLINE=92304974; PubMed=1610833;
 RA Dianoux A.-C., Stasia M.-J., Garin J., Gagnon J., Vignais P.V.;
 RT "The 23-kilodalton protein, a substrate of protein kinase C, in
 RT bovine neutrophil cytosol is a member of the S100 family.";
 RL Biochemistry 31:5898-5905(1992).
 RP [2]
 RN SEQUENCE OF 1-29.
 RC TISSUE=Esophageal epithelium;
 RX MEDLINE=93280230; PubMed=8505356;
 RA Tang T.-K., Hong T.-M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-J.,
 RA Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.-C.,
 RA Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;
 RT "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
 RT antibody W2 specifically reacts with condensed nuclei of
 RT differentiated superficial cells.";
 RL J. Cell Sci. 104:237-247(1993).
 CC -1- SUBUNIT: DISULFIDE LINKED HETERODIMER OF A 7/11 kDa AND A 22/23
 CC kDa SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC; LOOSELY ASSOCIATED TO THE
 CC CYTOSKELETON.
 CC -1- TISSUE SPECIFICITY: FOUND ESSENTIALLY IN PHAGOCYtic CELLS.
 CC -1- MISCELLANEOUS: BINDS TWO CALCIUM IONS PER MOLECULE WITH AN
 CC AFFINITY SIMILAR TO THAT OF THE S-100 PROTEINS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 DR PIR: B42628; B42628.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001751; S100_CaBP.
 DR Pfam: PF01023; S100; 1.
 DR PROSITE: PS00018; EF_HAND; PARTIAL.
 DR PROSITE: PS00303; S100_CaBP; PARTIAL.
 KM Calcium-binding.
 FT CA_BIND 20 33 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
 FT CONFLICT 10 11 DS -> NI (IN REF. 2).
 FT NON_TER 41 41
 SO SEQUENCE 41 AA; 4770 MW; 21C78BBF3ABDAB55 CRC64;

alignment_scores:
 Quality: 170.00 Length: 41
 Ratio: 4.595 Gaps: 0
 Percent Similarity: 90.244 Percent Identity: 78.049

alignment_block:

US-09-806-382A-1 x S108_BOVIN ..

Align seg 1/1 to: S108_BOVIN from: 1 to: 41

1 ATGTGACCGAGCTGGAGAAAGCCTTGACCTATCATCGACGCTACCA 50
 |||||
 1 Metleuthraspleuclu***AlaIleasperleuilepsvaltyrh 17
 51 CAACTACTCCCTGATTAAGGGGAAATTCATGCGCTACAGGAGTACC 100
 |||||
 17 slstyTyrSerleu***LysGlyAsnTyRHsAlaValtyr***Aspspl 34
 101 TGAAGAAATTCGTAGAGACCGAG 123
 |||||
 34 eulys***LeuIleucluthrclu 41

seq_name: SwissProt_40:M126_CHICK

seq_documentation_block:
 ID M126_CHICK STANDARD: PRT: 119 AA.
 AC P28318;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein MRP-126.
 DE Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WHITE LEGHORN; TISSUE=Bone marrow;
 RX MEDLINE=92195690; PubMed=1549365;
 RA Nakano T., Graf T.;
 RT "Identification of genes differentially expressed in two types of
 RT v-myb-transformed avian myelomonocytic cells.";
 RL Oncogene 7:527-534(1992).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN V-MYB-TRANSFORMED MYELOMONOCYTIC
 CC CELLS.
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X61200; -, NOT_ANNOTATED_CDS.
 DR HSSP: P04271; 10W0.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001751; S100_CaBP.
 DR Pfam: PF00036; ehand; 1.
 DR Pfam: PF01023; S100; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CaBP; 1.
 KM Calcium-binding.
 FT CA_BIND 29 42 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
 FT CA_BIND 72 83 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
 FT CONFLICT 119 14065 MW; 2D268DAF6309AD7A CRC64;
 SO SEQUENCE 119 AA; 14065 MW; 2D268DAF6309AD7A CRC64;

alignment_scores:
 Quality: 169.50 Length: 100
 Ratio: 2.457 Gaps: 2
 Percent Similarity: 69.000 Percent Identity: 36.000

alignment_block:

US-09-806-382A-1 x M126_CHICK ..

Align seg 1/1 to: M126_CHICK from: 1 to: 119

4 TTGACCGAGCTGGAGAAAGCCTTGACCTATCATCGACGCTACCA 53
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DR InterPro: IPR001751; S100_CaBP.
DR Pfam: PF00036; efnand, 1.
DR PFam: PF01023; S_100; 1.
DR PROSITE: PS00018; EF_HAND, 1.
DR PROSITE: PS00303; S100_CaBP; 1.
KW Calcium-binding; Zinc; Metal-binding.
FT INIT MET 0 0 BY SIMILARITY.
FT CA_BIND 18 31 EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY)
FT CA_BIND 61 72 EF-HAND 2 (HIGH AFFINITY) (BY SIMILARITY)
FT FT
SQ SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

alignment_scores:
Quality: 158.00 Length: 91
Ratio: 2.508 Gaps: 1
Percent Similarity: 69.231 Percent Identity: 36.264

alignment_block:
US-09-806-382A-1 x S112-BOVIN ..

Align seg 1/1 to: S112_BOVIN from: 1 to: 91

7 ACCGAGCGGGGAAGCGCTGACCTCATCATCGACGCTACCAAGTA 56
|||||
1 ThrLysLeuGlnAspHisLeuGlnGlyIleIleAsnIlePheHisGlnTy 17
57 CTCCCTGTAAGGGGGAATTTCATCCCTCATACAGGGATGACGTAAGA 106
|||||
17 rSerValArgValGlyHisPheAspHisPheAsnLysArgIleuLysG 34
107 AATTGCTAGAGACCGGAGTGTCTCATAGTATATCAG.....AAA 144
|||||
34 InLeuIleThrLysGlnLeuProLysThrLeuGlnAsnThrLysAspGln 50
145 AAGGTGACAGCGTCTGTGTCGAAGCTTGATATCAACACGATGATGTC 194
||||
51 ProThrIleAspLysIlePheGlnAspLeuAspAlaAspLysAspGlyAl 67
195 AGTTAACTTCCAGAGATTCTCATCTGCGTATGAAGAAGTGGCGTCGAC 244
|||||
67 aValSerPheGlnIuPheValIleuValIserArgValIleuLysThrA 84
245 CCCACAAAAAAGCCATGAAGAA 267
|||||
84 IaHisIleAspIleHisLysGln 91

seq_name: SwissProt_40:S109_BOVIN

seq_documentation_block:
ID S109_BOVIN STANDARD; PRT; 122 AA.
AC P28783;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calgranulin B (Neutrophil cytosolic 23 kDa protein) (P23) (BEE22)
DE (Fragment).
GN S100A9.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Oesophageal epithelium;
RX MEDLINE=93200230; PubMed=8505358;
RA Tang T.-M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-J.,
RA Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.J.-C.,
RA Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;
RA "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
RT antibody W2 specifically reacts with condensed nuclei of
RT differentiated superficial cells."

```

RL J. Cell Sci. 104:237-247(1993).
 RN [2]
 RN SEQUENCE OF 4-56.
 RC TISSUE-Neutrophils;
 RX MEDLINE-92304974; PubMed-1610833;
 RA Dianoux A.-C., Stasia M.-J., Garin J., Gagnon J., Vignais P.V.;
 RT "The 23-Kilodalton protein, a substrate of protein kinase C, in
 RT bovine neutrophil cytosol is a member of the S100 family.";
 RL Biochemistry 31:5898-5905(1992).
 CC -1 SUBUNIT: DISULFIDE LINKED HETERODIMER OF A 7/11 KDa AND A 22/23
 CC KDa SUBUNITS.
 CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC; LOOSELY ASSOCIATED TO THE
 CC CYTOSKELETON.
 CC -1 TISSUE SPECIFICITY: FOUND ESSENTIALLY IN PHAGOCYtic CELLS.
 CC -1 PTM: PHOSPHORYLATED BY PROTEIN KINASE C.
 CC -1 MISCELLANEOUS: CONTAINS TWO CA(2+)-BINDING DOMAINS PER PROTEIN.
 CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1 SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 DR HSP; P02638; IABO.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001751; S100_CaBP.
 DR Pfam: PF00036; efhand; 1.
 DR Pfam: PF01023; S_100; 1.
 DR PROSITE: PS00018; EF-HAND. PARTIAL.
 DR PROSITE: PS00303; S100_CaBP; 1.
 KM Calcium-binding; Phosphorylation.
 FT NON-TER 1 1
 FT CA_BIND 19 32 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
 FT CA_BIND 63 74 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
 SQ SEQUENCE 122 AA; 13673 MW; F3C8AC48806BECCD CRC64;

alignment_scores:
 Quality: 156.50 Length: 91
 Ratio: 2.236 Gaps: 1
 Percent Similarity: 76.923 Percent Identity: 27.473

alignment_block:

US-09-806-382a-1 x S109_BOVIN ..

Align seg 1/1 to: S109_BOVIN from: 1 to: 122

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4 TTGACCGAGCTGAGAAAGCCTTGAACTATCATCATGAGTCTACACAA 53
  ::::::::::::::::::::|::::::::::::::::::|:::
1 MeSeGmIcmeGluSeRserIleGluThrIleIleAsnIlePheHisel 17
54 GTACTCCCTGATAAAGGGAATTTCATGCCCTACAGGATGACCTGA 103
  ::::::::::::::::::::|::::::::::::::::::|:::
17 nTySeRvAlArgLeuGlyHisTyAspThrIleuIleGlnIlySgluPheL 34
104 AGAATTGCTAGAGACCGAGTGTCTCATATATCAGGAAAG..... 147
  ::::::::::::::::::::|::::::::::::::::::|:::
34 ySglInleuValGlnIlySgluLeuProAsnPhelIleuIlySglInIlyS 50
148 .....GGTGACAGCTGTGTTCAAGAGTTGGATATCAACACTGA 188
  ::::::::::::::::::::|::::::::::::::::::|:::
51 ASngulAlAlAlIleAsnGluIleMetGluAspLeuAspThrAsnValas 67
189 TGGTGAGTTAACTTCACAGAGTCTCATATCTGGTATGAAGAGGCG 238
  ::::::::::::::::::::|::::::::::::::::::|:::
67 pTySglInleuSerPheGluGluPheIleMetLeuValAlAlArgLeuThrV 84
239 TGGCAGCCCAAAAAAGCCAT 261
  ::::::::::::::::::::|
84 AlAlAserHisGluGluMetHis 91

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seq_name: SwissProt_40:S112_HUMAN

seq_documentation_block:
 ID S112_HUMAN STANDARD; PRT; 91 AA.
 AC P80511;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Calgranulin C (CGR) (P6) (CGR) (Neutrophil S100 protein) (Calcium-
 DE binding protein in amniotic fluid 1) (CAFL1) (p6).
 GN S100A12
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97138564; PubMed-8985590;
 RA Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;
 RT "Characterization of the human S100A12 (calgranulin C, p6, CAFL1,
 RT CGRP) gene, a new member of the S100 gene cluster on chromosome
 RL 1q21.";
 RN Cell Calcium 20:459-464(1996).
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96192053; PubMed-8619860;
 RA Yamamura T., Hiltom J., Nagasaki K., Suzuki M., Takahashi E.,
 RA Saito S., Tsukada T., Yamaguchi K.;
 RT "Human CAFL1 gene -- molecular cloning, gene structure, and chromosome
 RT mapping.";
 RN Biochem. Biophys. Res. Commun. 221:356-360(1996).
 RP SEQUENCE.
 RX MEDLINE-96192069; PubMed-8619876;
 RA Marti T., Ertmann K.D., Gallin M.Y.;
 RT "Host-parasite interaction in human onchocerciasis: identification
 RT and sequence analysis of a novel human calgranulin.";
 RL Biochem. Biophys. Res. Commun. 221:454-458(1996).
 RN [4]
 RP SEQUENCE.
 RC TISSUE-Neutrophils;
 RX MEDLINE-96332419; PubMed-8769108;
 RA Iig E.C., Troxler H., Buerigisser D.M., Kuster T., Markert M.,
 RA Guignard F., Hunziker P., Bircher N., Heizmann C.W.;
 RT "Amino acid sequence determination of human S100A12 (p6, calgranulin
 RT C, CGRP, CAFL1) by tandem mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
 RN [5]
 RP SEQUENCE OF 1-20.
 RX MEDLINE-95351965; PubMed-7626002;
 RA Guignard F., Manuel J., Markert M.;
 RT "Identification and characterization of a novel human neutrophil
 RT protein related to the S100 family.";
 RL Biochem. J. 309:395-401(1995).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
 RX MEDLINE-21065388; PubMed-11134923;
 RA Moroz O.V., Antson A.A., Murshudov G.N., Maitland N.J., Dodson G.G.,
 RA Wilson K.S., Skibshoj I., Luknadin E.M., Bronstein I.B.;
 RT "The three-dimensional structure of human S100A12.";
 RL Acta Crystallogr. D 57:20-29(2001).
 CC -1 SUBUNIT: HOMODIMER.
 CC -1 TISSUE SPECIFICITY: MONOCYTES AND LYMPHOCYTES.
 CC -1 MASS SPECTROMETRY: MW=10444; METHOD=Electrospray.
 CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1 SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL: X98290; CA94792.1; JOINED.
 DR EMBL: D49549; BAA08497.1; -
 DR EMBL: D83664; BAA12036.1; -
 DR EMBL: D83657; BAA12030.1; -
 DR PDB: 1E8A; 08-JAN-01.
 DR MIM: 603112; -
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001751; S100_CaBP.
 DR Pfam: PF00036; ehand; 1.
 DR Pfam: PF01023; S_100; 1.
 DR PROSITE: PS00018; EF_HAND; FALSE_NEG.
 DR PROSITE: PS00303; S100_CaBP; 1.
 DR Calcium binding; Zinc; Metal-binding; 3D-structure.
 FT INIT_MEF 0
 FT CA_BIND 18 31 EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY).
 FT CA_BIND 61 72 EF-HAND 2 (HIGH AFFINITY) (BY SIMILARITY).
 FT SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;

alignment_scores:

Quality: 156.00 Length: 95
 Ratio: 2.516 Gaps: 2
 Percent Similarity: 65.263 Percent Identity: 38.947

alignment_block:

US-09-806-382a-1 x S112_HUMAN ..

Align seg 1/1 to: S112_HUMAN from: 1 to: 91

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7  ACCGACCTGGAGAAAGCCTGGAACCTATACATCGACGCTACCAACAGTA 56
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
1  ThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnIty 17
57  CTCCTCATTAAGAGGGAATTTTCATGCGCTACAGGAGTACGACATGAGA 106
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
17  rserValArgLysGlyHisPheAspThrLeuSerLysGlyIleuLysG 34
107  AATTGCTAGAGACCGAGTCTCCATCATATATACG.....AAA 144
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||
34  ILeuLeuThrLysGlyIleuAlaAsnThrIleLysAsnIleLysAspLys 50
145  AAGGCTGCAGACGCTGTGTTCAAGAGTTGATCAACACATGATGATGCTC 194
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
51  AlAlaValIleAspGluIlePheGlnGlyLeuAspAlaAsnGlnAspGlu 67
195  AGTTAACTTCAGAGAGTTCCTCATTCGTGCTATAAAGATGGCGCTGCAG 244
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
67  nValAspPheGlnGluPheIleSerLeuVal.....AlaIleA 80
245  CCCACAAAAAAGCCATGAAAGAACCCACAAAGAG 279
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
80  ILeuLysAlaIleHisTyrHisThrHisLysGlu 91

```

seq_name: SwissProt_40:S10E_HUMAN

seq_documentation_block:

ID S10E_HUMAN STANDARD; PRT; 95 AA.
 AC P25815;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE S100P protein.
 GN S100P OR S100E.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92339442; PubMed=1633809;
 RA Becker T., Gerke V., Kube E., Weber K.;

RT "S100P, a novel Ca(2+)-binding protein from human placenta. cDNA
 RT cloning, recombinant protein expression and Ca2+ binding
 RT properties.";
 RL Eur. J. Biochem. 207:541-547(1992).
 RN [2]

RP SEQUENCE OF 1-91.
 RC TISSUE=Placenta;
 RX MEDLINE=92171935; PubMed=1540168;
 RA Emoto Y., Kobayashi R., Akatsuka H., Hidaka H.:
 RT "Purification and characterization of a new member of the S-100
 RT protein family from human placenta.";
 RL Biochem. Biophys. Res. Commun. 182:1246-1253(1992).
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM IONS.
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to [license@isb-sid.ch](mailto:license@isb-sib.ch)).
 CC -----

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DR EMBL: X65614; CAA46566.1; -
DR PIR: S24146; S24146.
DR HSSP: P02638; 1CFP.
DR MIM: 600614; -
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_CaBP.
DR Pfam: PF00036; ehand; 1.
DR Pfam: PF01023; S_100; 1.
DR PROSITE: PS00018; EF_HAND; FALSE_NEG.
DR PROSITE: PS00303; S100_CaBP; 1.
KW Calcium-binding; Placenta.
FT CA_BIND 19 32 EF-HAND 1 (LOW AFFINITY).
FT CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY).
FT CONFLICT 32 32 E -> T (IN REF. 2).
FT CONFLICT 44 44 F -> E (IN REF. 2).
FT SEQUENCE 95 AA; 10400 MW; 786E6E3FE3EAC6C61 CRC64;

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alignment_scores:

Quality: 154.00 Length: 87
 Ratio: 2.525 Gaps: 1
 Percent Similarity: 70.115 Percent Identity: 37.931

alignment_block:

US-09-806-382a-1 x S10E_HUMAN ..

Align seg 1/1 to: S10E_HUMAN from: 1 to: 95

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4  TTGACCGAGTGGAGAAAGCCTGGAACCTATCATGCGCTACACACAA 53
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
1  MethTrGluLeuGluThrAlaMetGlyMetIleLeuAspValPheSerAr 17
54  GTACTCCCTGATTAAGGGAATTTCCATGCGCTACAGGATGACCTGTA 103
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||
17  gTyrSerGlySerGluGlySerThrGlnThrLeuThrLysGlyIleuLeu 34
104  AGAATGCTAGAGACGAGCGAGTGCCTCAGTATATACAG..... 141
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
34  yValIleuMetGlnLysGluLeuProGlyPheLeuGlnSerGlyLysASP 50
142  AAAAAGGCTGCAGACGCTGTGTTCAAGAGTTGATATCAACACTGATGG 191
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
51  LysAspAlaValAspLysLeuLeuLysAspLeuAspAlaAsnGlnAspAl 67
192  TGCAGTTAACTTCAGAGAGTTCCTCATTCGTGCTATAAAGATGGCGCTG 241
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||
67  aGlnValAspPheSerGluPheIleValAlaIleAlaIleThrSerA 84
242  CAGCCACAA 252

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||||:|||||
84 lacysHsLys 87

seq_name: SwissProt_40:S112_PIG

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seq_documentation_block:
ID   S112_PIG          STANDARD;          PRT;          91 AA.
AC   P80310;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Calgranulin C (CAGC).
GN   S100A12.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9623;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Granulocyte;
RX   MEDLINE=95050708; PubMed=7961855;
RA   Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
RT   Primary structure and binding properties of calgranulin C, a novel
RT   S100-like calcium-binding protein from pig granulocytes.";
RL   J. Biol. Chem. 269:28929-28936(1994).
CC   -1- TISSUE SPECIFICITY: FOUND ESSENTIALLY IN GRANULOCYTES WITH SMALL
CC   AMOUNTS FOUND IN LYMPHOCYTES.
CC   -1- MISCELLANEOUS: IN THE ABSENCE OF ZINC BINDS ONE CALCIUM ION PER
CC   MOLECULE. IN THE PRESENCE OF ZINC BINDS TWO CALCIUM IONS PER
CC   MOLECULE.
CC   -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC   -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
DR   HSSP: P02632; ICBL
DR   InterPro: IPR002048; EF-hand
DR   InterPro: IPR001751; S100_Cabp.
DR   Pfam: PF00036; ehand; 1.
DR   PROSITE: PS00036; S100_CABP; 1.
DR   PROSITE: PS00033; S100_CABP; 1.
KM   Calcium-binding; zinc; metal-binding.
FT   CA_BIND 18 31 EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY).
FT   CA_BIND 61 72 EF-HAND 2 (HIGH AFFINITY) (BY
FT   CA_BIND 10614 10614 MW; BA204461A32D7FCE CRC64;
SO   SEQUENCE

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alignment_scores:
Quality: 151.00 Length: 91
Ratio: 2.323 Gaps: 2
Percent Similarity: 71.429 Percent Identity: 35.165

alignment_block:
US-09-806-382a-1 x S112_PIG ..

Align seg 1/1 to: S112_PIG from: 1 to: 91

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7  ACCGAGCTGGAGAAGCCCTGAACCTGATACGAGCTACACAGTA 56
||||:||||| |||:||||| |||:||||| |||:|||||
1  TTTTSTLGLGLASPHISLGLUGLGLTLEIISNIILEPHNISGLNTY 17
57  CTCCCTGATAAAGGGAATTTCCATGCCCTCTACAGGAGTGAAGTGA 106
||||:||||| |||:||||| |||:||||| |||:|||||
17  rserValaLgLeuGLyHISLTYAspHrLeuLeuLysArGluLeuLysG 34
107  AATTGCTAGAGACCGAGTCTCTCACTATATCAGGAAA.....AAG 147
||||:||||| |||:||||| |||:||||| |||:|||||
34  InLeuIleHrLysGLuLeuProAsnThrLeuLysAsnThrLysAspGln 50
148  GGTGCA...GAGCTGCTTCAAGAGTGAATATCAACACAGATGTTGC 194
||||:||||| |||:||||| |||:||||| |||:|||||
51  GLYTHrILeAspLysILePhnGLnSLnLeuAspAlaSLnGLnAspELucl 67
195  AGTAACTTCAGAGAGTTCCTATTCGTGATTAAGATGGCGCTGGCAG 244

```

||||:||||| |||:||||| |||:||||| |||:|||||
67 nValSerPhnLysGLuPhnValValLeuValHrAspValLeuIleHrThra 84
84 IaHISAspAsnIleHISLysGLu 91

seq_name: SwissProt_40:S10A_RAT

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seq_documentation_block:
ID   S10A_RAT          STANDARD;          PRT;          93 AA.
AC   P35467;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   S-100 protein, alpha chain.
GN   S100A1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RA   Song W.;
RT   Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.
RN   [2]
RP   SEQUENCE OF 10-93 FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=92076235; PubMed=1742602;
RA   Zimmer D.B., Song W., Zimmer W.E.;
RT   Isolation of a rat S100 alpha cDNA and distribution of its mRNA in
RT   rat tissues.";
RL   Brain Res. Bull. 27:157-162(1991).
CC   -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-
CC   DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
CC   IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
CC   ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
CC   AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
CC   -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
CC   ONE ALPHA AND ONE BETA CHAIN.
CC   -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
CC   BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.
CC   -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC   -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
-----
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CC   or send an email to license@isb-sib.ch).
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CC   EMBL: U26358; AAB53657.1; -.
CC   EMBL: U26357; AAB53657.1; JOINED.
CC   EMBL: S68809; AAB20539.2; -.
CC   HSSP: P04631; 1B4C.
CC   InterPro: IPR002048; EF-hand.
CC   InterPro: IPR001751; S100_Cabp.
CC   Pfam: PF00036; ehand; 1.
CC   Pfam: PF01023; S_100; 1.
CC   PROSITE: PS00018; EF_HAND; 1.
CC   PROSITE: PS00033; S100_CABP; 1.
DR   PROSITE: PS00033; S100_CABP; 1.
KM   Calcium-binding; zinc; metal-binding.
FT   CA_BIND 0 0 EF-HAND 1 (LOW AFFINITY).
FT   CA_BIND 19 32 EF-HAND 2 (HIGH AFFINITY).
FT   CA_BIND 62 73 N -> H (IN REF. 2).
FT   CONFLICT 13 13 K -> R (IN REF. 2).
FT   CONFLICT 56 56
SO   SEQUENCE 93 AA; 10429 MW; D2959A95EC0651A9 CRC64;

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alignment_scores:
  Quality: 148.00      Length: 92
  Ratio: 2.277        Gaps: 2
  Percent Similarity: 70.652      Percent Identity: 39.130

alignment_block:
US-09-806-382a-1 x S10A_RAT ..

Align seg 1/1 to: S10A_RAT from: 1 to: 93

7 ACCGAGCTGGAGAAAGCCTTGAACCTATCATGACGCTCTACCAAGCA 56
  ::::::::::::::::::::|::::::::::::::::::|:::
2 SERGLULEUGLINTHRAlaMetGluThrLeuIleAsnValPheHisAlaH1 18
  ::::::::::::::::::::|::::::::::::::::::|:::
57 CTCCTGATTAAGGAGGAAATTCATCCGCTTCACAGGATGACGTGAAGA 106
  ::::::::::::::::::::|::::::::::::::::::|:::
18 sSerGlyLysGluGlyAspLysTyrLysLeuSerLysLysGluLeuLysA 35
  ::::::::::::::::::::|::::::::::::::::::|:::
107 AATTCGTAGAGACCGAGTGTCTCTCAGTATATCAGC...AAAAAGGTGCA 153
  ::::::::::::::::::::|::::::::::::::::::|:::
35 sPLeuLeuGlnThrGluLeuSerPheLeuAspValGlnLysAspAla 51
  ::::::::::::::::::::|::::::::::::::::::|:::
154 GACGTC.....TGGTCAAGAGTTGATATCAACACTGATGAGTGC 194
  ::::::::::::::::::::|::::::::::::::::::|:::
52 AspAlaValAspLysIleMetLysGluLeuAspGluAsnGlyAspGlyG1 68
  ::::::::::::::::::::|::::::::::::::::::|:::
195 AGTTAACTTCACAGAGTTCCTCATTCGTGGTAAAGATGGCGGTGCAG 244
  ::::::::::::::::::::|::::::::::::::::::|:::
68 uValAspPheGlnGluPheValIleValAlaIleAlaLeuThrValAlaC 85
  ::::::::::::::::::::|::::::::::::::::::|:::
245 CCCACAAAAAAGCCATGAAGAAAGC 270
  ::::::::::::::::::::|::::::::::::::::::|:::
85 ysAsnAsnPhePheTrpGluAsnSer 93
  ::::::::::::::::::::|::::::::::::::::::|:::

seq_name: SwissProt_40:S10A_BOVIN
seq_documentation_block:
ID S10A_BOVIN STANDARD; PRT; 93 AA.
AC P02639;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE S-100 protein, alpha chain.
GN S100A1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86248083; PubMed=3755105;
RA Kuwano R., Maeda T., Usui H., Araki K., Yamakuni T., Ohshima Y.,
RA Kurihara T., Takahashi Y.;
RT "Molecular cloning of cDNA of S100 alpha subunit mRNA.";
RL FEBS Lett. 202:97-101(1986).
RN [2]
RP SEQUENCE.
RX MEDLINE=81236562; PubMed=7250124;
RA Itohe T., Okuyama T.;
RT "The amino-acid sequence of the alpha subunit in bovine brain S-100a
RT protein.";
RL Eur. J. Biochem. 116:79-86(1981).
RN [3]
RP METAL ION-BINDING PROPERTIES.
RX MEDLINE=84000339; PubMed=6615778;
RA Baudier J., Gerard D.;
RT "Ions binding to S100 proteins: structural changes induced by calcium
RT and zinc on S100a and S100b proteins.";
RL Biochemistry 22:3360-3369(1983).
CC -I- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-
CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH

```

```

CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
CC ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
CC -I- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
CC ONE ALPHA AND ONE BETA CHAIN.
CC -I- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.
CC -I- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -I- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
DR PIR; A24156; A24156.
DR PIR; A03078; BCBOIA.
DR HSSP; P04631; 1B4C.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_CABP.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; zinc; Metal-binding.
FT INIT_MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT CA_BIND 19 32 EF-HAND 1 (LOW AFFINITY).
FT CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY).
FT CONFLICT 64 64 N -> D (IN REF. 2).
SQ SEQUENCE 93 AA; 10387 MW; 0457D0F44819B89B CRC64;

alignment_scores:
  Quality: 146.00      Length: 92
  Ratio: 2.246        Gaps: 2
  Percent Similarity: 70.652      Percent Identity: 38.043

alignment_block:
US-09-806-382A-1 x S10A_BOVIN ..

Align seg 1/1 to: S10A_BOVIN from: 1 to: 93

7 ACCGAGCTGGAGAAAGCCTTGAACCTATCATGACGCTCTACCAAGCA 56
  ::::::::::::::::::::|::::::::::::::::::|:::
2 SERGLULEUGLINTHRAlaMetGluThrLeuIleAsnValPheHisAlaH1 18
  ::::::::::::::::::::|::::::::::::::::::|:::
57 CTCCTGATTAAGGAGGAAATTCATCCGCTTCACAGGATGACGTGAAGA 106
  ::::::::::::::::::::|::::::::::::::::::|:::
18 sSerGlyLysGluGlyAspLysTyrLysLeuSerLysLysGluLeuLysG 35
  ::::::::::::::::::::|::::::::::::::::::|:::
107 AATTCGTAGAGACCGAGTGTCTCTCAGTATATC...AGAAAAAGGTGCA 153
  ::::::::::::::::::::|::::::::::::::::::|:::
35 luleuLeuGlnThrGluLeuSerGlyPheLeuAspAlaGlnLysAspAla 51
  ::::::::::::::::::::|::::::::::::::::::|:::
154 GACGTC.....TGGTCAAGAGTTGATATCAACACTGATGTCG 194
  ::::::::::::::::::::|::::::::::::::::::|:::
52 AspAlaValAspLysValMetLysGluLeuAspGluAsnGlyAspGlyG1 68
  ::::::::::::::::::::|::::::::::::::::::|:::
195 AGTTAACTTCACAGAGTTCCTCATTCGTGGTAAAGATGGCGGTGCAG 244
  ::::::::::::::::::::|::::::::::::::::::|:::
68 uValAspPheGlnGluPheValIleValAlaIleAlaLeuThrValAlaC 85
  ::::::::::::::::::::|::::::::::::::::::|:::
245 CCCACAAAAAAGCCATGAAGAAAGC 270
  ::::::::::::::::::::|::::::::::::::::::|:::
85 ysAsnAsnPhePheTrpGluAsnSer 93
  ::::::::::::::::::::|::::::::::::::::::|:::

seq_name: SwissProt_40:S10A_HUMAN
seq_documentation_block:
ID S10A_HUMAN STANDARD; PRT; 93 AA.
AC P23297;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE S-100 protein, alpha chain (S100 calcium-binding protein A1).
GN S100A1 OR S100A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



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FT      CONFLICT      21      21      Q -> E (IN AA207749)
FT      CONFLICT      21      21      Q -> M (IN AA500563)
FT      CONFLICT      21      21      Q -> H (IN AA432539)
FT      CONFLICT      21      21      Q -> K (IN REF. 2)
SQ      SEQUENCE      93 AA; 10374 MW; C969E39EAI8D/05C CRC64;

alignment_scores:
  Quality: 139.00      Length: 92
  Ratio: 2.172      Gaps: 2
  Percent Similarity: 69.565      Percent Identity: 36.957

alignment_block:
US-09-806-382A-1 x S10A_MOUSE ..

Align seg 1/1 to: S10A_MOUSE from: 1 to: 93

7 ACCGAGCTGGAGAAAGCCTTGACCTATCATCGACGTACACCAAGTA 56
  :::::::::::::::::::::::::::::::::::::::::::::::
2 SerGluLeuGluSerAlaMetGluThrLeuIleAsnValPheHisAlaH1 18
  :::::::::::::::::::::::::::::::::::::::::::::::
57 CTCCTGATTAAGGGAATTCATGCCCTCTACAGGATGACCTGAAGA 106
  :::::::::::::::::::::::::::::::::::::::::::::::
18 sSerGlyGlnGlyAspLysTyrLysLeuSerLysLysGluLeuLysA 35
  :::::::::::::::::::::::::::::::::::::::::::::::
107 AATTGCTAGACCGGAGTGTCTCTCATATATACAG...AAAAAGGTGCA 153
  :::::::::::::::::::::::::::::::::::::::::::::::
35 spleuLeuGlnThrGluLeuSerGlyPheLeuAspValGlnIlnAspAla 51
  :::::::::::::::::::::::::::::::::::::::::::::::
154 GAGCTC.....TGTTCAAGAGATTGATATCAACATGATGATGCTC 194
  :::::::::::::::::::::::::::::::::::::::::::::::
52 AspAlaValAspLysValMetLysGluLeuAspGluAsnGlyAspGlyG1 68
  :::::::::::::::::::::::::::::::::::::::::::::::
195 AGTTAACTCCAGAGATTCCTCATTCGTGTGATTAAGATGGCGGTGAC 244
  :::::::::::::::::::::::::::::::::::::::::::::::
68 uValAspPheLysGluTyrValValLeuValAlaIleuThrValAlaIac 85
  :::::::::::::::::::::::::::::::::::::::::::::::
245 CCCACAAAAGCCATGAGAAAGC 270
  :::::::::::::::::::::::::::::::::::::::::::::::
85 yAsnAsnPhePheThrGluThrSer 93

seq_name: SwissProt_40:S10B_BOVIN

seq_documentation_block:
ID      S10B_BOVIN      STANDARD;      PRT;      91 AA.
AC      P02638;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      S-100 protein, beta chain.
GN      S100B.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=79045265; PubMed=710399;
RA      "Isobe T., Okuyama T.;"
RT      "The amino-acid sequence of S-100 protein (PAP I-b protein) and its
RL      relation to the calcium-binding proteins.;"
RL      Eur. J. Biochem. 89:379-388(1978).
RN      [2]
RP      REVIEWS TO 1-4.
RX      MEDLINE=81236562; PubMed=7250124;
RA      "Isobe T., Okuyama T.;"
RT      "The amino-acid sequence of the alpha subunit in bovine brain S-100a
RL      protein.;"
RL      Eur. J. Biochem. 116:79-86(1981).
RN      [3]
RP      SEQUENCE.

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RX      MEDLINE=85278169; PubMed=4026304;
RA      Marshak D.R., Umekawa H., Watterson D.M., Higaka H.;"
RT      "Structural characterization of the calcium binding protein s100 from
RT      adipose tissue.;"
RL      Arch. Biochem. Biophys. 240:777-780(1985).
RN      [4]
RP      METAL ION-BINDING PROPERTIES.
RX      MEDLINE=84000339; PubMed=6615778;
RA      Baudier J., Gerard D.;"
RT      "Ions binding to S100 proteins: structural changes induced by calcium
RT      and zinc on S100a and S100b proteins.;"
RL      Biochemistry 22:3360-3369(1983).
RN      [5]
RP      CADMIUM-BINDING STUDIES.
RX      MEDLINE=91248136; PubMed=2039467;
RA      Donato H. Jr., Mani R.S., Kay C.M.;"
RT      "Spectral studies on the cadmium-ion-binding properties of bovine
RT      brain S-100b protein.;"
RL      Biochem. J. 276:13-18(1991).
RN      [6]
RP      STRUCTURE BY NMR.
RX      MEDLINE=96398693; PubMed=8805590;
RA      Kilby P.M., van Eldik L.J., Roberts G.C.K.;"
RT      "The solution structure of the bovine S100b protein dimer in the
RT      calcium-free state.;"
RL      Structure 4:1041-1052(1996).
CC      -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-
CC      DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
CC      IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
CC      ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
CC      AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
CC      -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
CC      ONE ALPHA AND ONE BETA CHAIN.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
CC      BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.
CC      -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC      -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
DR      PIR; A03077; BCB01B.
DR      PDB; 1CFP; 12-MAR-97.
DR      PDB; 1MHO; 18-NOV-98.
DR      InterPro; IPR002048; EF-hand.
DR      InterPro; IPR001751; S100_CABP.
DR      Pfam; PF00036; efhand; 1.
DR      Pfam; PF01023; S_100; 1.
DR      PROSITE; PS00018; EF_HAND; 1.
DR      PROSITE; PS00303; S100_CABP; 1.
KW      Calcium-binding; zinc; Metal-binding; Acetylation; 3D-structure.
FT      MOD_RES      1      1      ACETYLATION.
FT      CA_BIND      18      31      EF-HAND 1 (LOW AFFINITY).
FT      CA_BIND      61      72      EF-HAND 2 (HIGH AFFINITY).
SQ      SEQUENCE      91 AA; 10537 MW; 386201933DB93A CRC64;

alignment_scores:
  Quality: 137.00      Length: 86
  Ratio: 2.210      Gaps: 1
  Percent Similarity: 72.093      Percent Identity: 33.721

alignment_block:
US-09-806-382A-1 x S10B_BOVIN ..

Align seg 1/1 to: S10B_BOVIN from: 1 to: 91

7 ACCGAGCTGGAGAAAGCCTTGACCTATCATCGACGTACACCAAGTA 56
  :::::::::::::::::::::::::::::::::::::::::::::::
1 SerGluLeuGlnLysAlaValAlaLeuIleAspValPheHisGlnTyr 17
  :::::::::::::::::::::::::::::::::::::::::::::::
57 CTCCTGATTAAGGGAATTCATGCCCTCTACAGGATGACCTGAAGA 106
  :::::::::::::::::::::::::::::::::::::::::::::::
17 rSerGlyArgGlnGlyAspLysHisLysLeuLysSerGluLeuLysG 34
  :::::::::::::::::::::::::::::::::::::::::::::::
107 AATTGCTAGACCGGAGTGTCTCTCATATATC.....ACGAAA 144

```

```
34  IuLeuIleAsnAsnGluLeuSerHisPheLeuGluGluIleLysGluGln 50
    ::|||:.....|||  :::::
145 AAGGTCGACAGCTCTGGTCAAGAGTTGATATCAACACTGATGTC 194
    ::  ::|||  ::::: |||||  ::  |||||
51 GluValValAspLysValMetGluThrLeuAspSerAspGlyAspGlyG1 67
    ::|||:|||||:|||||:  ::|||
195 AGTTAACTTCACAGAGTTCTCATCTGTGATGAATAAGATGGCGTGCAG 244
    ::|||:|||||:|||||:  ::|||
67 uCysAspPheGlnGluPheMetAlaPheValAlaMetIleThrThrAlaC 84
    ::|||:|||||:|||||:  ::|||
245 CCCACAAA 252
84 ySHISGlu 86
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OM of: US-09-806-382a-1 to: SPREMBL_19:* out_format : pfs
Date: Sep 9, 2002 3:24 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framer_n2p.model -DEV=xlp
-O=/cgn2_1/USPRO_pool/US09806382/runatc_09092002_143849_15535/app-query.fasta_1.752
-DB=SPREMBL_19 -OFMT=fasta -SUFFIX=rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOF=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blotsum62
-TRANS=human40.cdi -LIST=45 -DGCALIGN=200 -THR_SCORE=Pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09806382.@CGNL.1.279 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-806-382a-1
Query length: 282
Database: SPREMBL_19:*
Database sequences: 56222
Database length: 172994929
Search time (sec): 104.890000

Score list:

Sequence	Strd	Orig	ZScore	Escore	Len	Documentation
SP_mammal:Q28714	+	269.50	584.94	4.3e-24	73	Q28714 oryctolagus cuniculus (rat)
SP_vertibrate:093395	+	146.00	312.10	2.6e-08	101	Q93395 salvelinus fontinalis (fish)
SP_rodent:Q9D3M4	+	140.00	299.63	2.6e-08	94	Q9D3M4 mus musculus (mouse). s10
SP_rodent:Q91V77	+	140.00	299.63	2.6e-08	94	Q91V77 m. 11 days embryo cdna, rat
SP_human:Q9H4U7	+	139.00	308.64	2.8e-08	92	Q9H4U7 homo sapiens (human). cal
SP_rodent:Q925J3	+	139.00	297.63	3.4e-08	92	Q925J3 cricetus griseus (chinese)
SP_rodent:Q9JL08	+	135.00	290.26	1.0e-07	79	Q9JL08 mus musculus (mouse). s10
SP_mammal:Q9TV56	+	127.00	270.57	1.0e-06	101	Q9TV56 canis familiaris (dog). s10
SP_human:Q9H4U7	+	126.00	264.12	1.5e-06	95	Q9H4U7 homo sapiens (human). tu
SP_human:Q9H4U7	+	125.50	266.20	1.5e-06	114	Q9H4U7 homo sapiens (human). tu
SP_human:Q9H4U7	+	125.00	262.73	1.4e-06	25	Q9H4U7 homo sapiens (human). mi
SP_human:Q9H4U7	+	122.00	252.94	4.5e-06	213	Q9H4U7 homo sapiens (human). cal
SP_human:Q9H4U7	+	118.50	232.26	1.1e-05	98	Q9H4U7 homo sapiens (human). s10
SP_human:Q9H4U7	+	114.50	227.39	4.3e-05	591	Q9H4U7 homo sapiens (human). fi
SP_human:Q9H4U7	+	114.50	226.04	4.4e-05	687	Q9H4U7 homo sapiens (human). d
SP_human:Q9H4U7	+	112.00	219.81	5.6e-05	1218	Q9H4U7 homo sapiens (human). d
SP_vertibrate:09PSF6	+	109.00	232.36	0.0002	89	Q9PSF6 ratelurus punctatus (chinese)
SP_rodent:Q9R2B7	+	107.00	230.15	0.0003	70	Q9R2B7 ratelurus punctatus (chinese)
SP_human:Q9H4U7	+	105.50	223.40	0.0004	103	Q9H4U7 bos taurus (bovine). com
SP_rodent:Q91X65	+	105.00	224.58	0.0005	80	Q91X65 mus musculus (mouse). s10
SP_human:Q9H4U7	+	100.00	226.09	0.0015	20	Q9H4U7 mus musculus (human). cal
SP_rodent:Q9D708	+	100.00	209.72	0.0020	124	Q9D708 mus musculus (mouse). 23
SP_vertibrate:09YH57	+	98.50	201.41	0.0033	217	Q9YH57 rana catesbeiana (bullfrog)
SP_human:Q9H4U7	+	97.50	207.23	0.0038	89	Q9H4U7 homo sapiens (human). psc
SP_rodent:Q9H4U7	+	96.00	213.71	0.0049	30	Q9H4U7 ratelurus punctatus (chinese)
SP_human:Q9H4U7	+	91.00	206.42	0.0188	20	Q9H4U7 homo sapiens (human). on
SP_rodent:Q9D3P1	+	88.00	168.78	0.0736	638	Q9D3P1 mus musculus (mouse). 54
SP_plant:Q9S531	+	84.50	171.15	0.1659	209	Q9S531 arabidopsis thaliana (md)
SP_invertebrate:077372	+	84.50	147.69	0.2680	4981	Q77372 plasmidium talchiptum (md)
SP_plant:Q9IKN1	+	83.50	160.26	0.2543	551	Q9IKN1 gossypium hirsutum (upland)
SP_rodent:Q9H4U7	+	81.50	112.88	0.3346	83	Q9H4U7 ratelurus punctatus (chinese)
SP_plant:Q9H4U7	+	81.00	154.77	0.5128	553	Q9H4U7 arabidopsis thaliana (md)
SP_plant:Q9S5W7	+	79.50	152.25	0.7708	508	Q9S5W7 gossypium arboreum (upland)
SP_bacteriap:Q9H4U7	+	74.50	154.35	2.51	119	Q9H4U7 mycoplasma pulmonis (hyp)
SP_invertebrate:Q9H4U7	+	74.50	149.42	2.73	206	Q9H4U7 drosophila melanogaster
SP_invertebrate:Q9H4U7	+	74.00	149.06	3.10	190	Q9H4U7 naegleria fowleri (amoeba)
SP_invertebrate:Q9H4U7	+	74.00	144.38	3.36	320	Q9H4U7 caenorhabditis elegans
SP_plant:Q9S5W4	+	74.00	138.81	3.69	595	Q9S5W4 dunaliella tertiolecta
SP_plant:Q9S5W5	+	74.00	135.10	3.93	900	Q9S5W5 arabidopsis thaliana (md)

SP_human:Q96K91 + 73.50 143.46 3.85 314 Q96K91 homo sapiens (human).
SP_invertebrate:Q9V214 + 73.50 140.76 4.03 424 Q9V214 drosophila melanogaster
SP_invertebrate:Q9VXU1 + 73.00 129.65 5.49 1294 Q9VXU1 drosophila melanogaster
SP_invertebrate:Q960D0 + 73.00 128.96 5.56 1398 Q960D0 drosophila melanogaster
SP_plant:Q9S168 + 72.50 125.63 6.64 1794 Q9S168 arabidopsis thaliana

seq_name: SP_mammal:Q28714

seq_documentation_block:
ID Q28714 PRELIMINARY; PRT: 73 AA.
AC Q28714:
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MACROPHAGE MIGRATION INHIBITORY FACTOR-RELATED PROTEIN-8
DE (FRAGMENT).
GN MRP-8.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE.
RX MEDLINE=94198229; PubMed=8148323;
RA Mori S., Goto K., Goto F., Murakami K., Ohkawara S., Yoshinaga M.;
RT "Dynamic changes in mRNA expression of neutrophils during the course
RT of acute inflammation in rabbits";
RL Int. Immunol. 6:149-156(1994).
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL: D17405; BAA04228.1; -.
DR HSSP: P02632; ICB1.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_CABP.
DR Pfam: PF01023; S_100; 1.
FT NON_TER 73
SQ SEQUENCE 73 AA; 8381 MW; F69089226601A163 CRC64;

alignment_scores:

Quality: 269.50 Length: 74
Ratio: 4.278 Gaps: 1
Percent Similarity: 85.135 Percent Identity: 74.324

alignment_block:

US-09-806-382a-1 x Q28714

Align seg 1/1 to: Q28714 from: 1 to: 73

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1 ATGTTGACCGAGCTGGAGAAAGCTTAACCTATATCATGACGCTACCA 50
|||||
1 MetProthraspleuGuasnserrleuAsnserrlellepheValtyrH 17
51 CAACTACTCCCTGATTAAGGGAATTCATGCCGCTACAGGAGGAC 100
|||||
17 SlvsCysSerleuclulysnryrGlnAlaLeuTy...GlyAsp 33
101 TGAAGAAATGCTAGAGACGAGTGTCTCAGATATACAGAAAGGCT 150
|||||
33 eulysleuLeuAlaThrlGlyCysproclnrySerlyslvsAsp 49
151 GCAGACGCTGCTTCAAGAGCTTGATATACACGTGATGCTCACTTAA 200
|||||
50 AlaspserrTrpPhelysGluLeuAspIleasnsrAspelyslaseras 66
201 CTTCCAGAGTCTCTCATCTCTG 222
|||||
66 nphelnglnclupheuleuLeu 73
seq_name: SP_vertibrate:Q93395
seq_documentation_block:
ID Q93395 PRELIMINARY; PRT: 101 AA.
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AC 093395;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE S100-LIKE CALCIUM BINDING PROTEIN.
 GN S100.
 OS Salvelinus fontinalis (Brook trout) (Brook char).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OX NCBI_TaxID=8038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVULATORY OVARY;
 RX MEDLINE=20534789; PubMed=11080585;
 RA Bohe J., Goetz F.W.;
 RT "A S100 homologue mRNA isolated by differential display PCR is down-
 regulated in the brook trout (Salvelinus fontinalis) post-ovulatory
 RT ovary";
 RL Gene 257,187-194(2000).
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 DR EMBL; AF077613; AAC28367.1; -
 DR HSSP; P02633; 4ICB.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001751; S100_CABP.
 DR Pfam; PF00036; ehand.1.
 DR Pfam; PF01023; S_100; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00303; S100_CABP; 1.
 KW Calcium-binding.
 SQ SEQUENCE 101 AA; 11285 MW; BF45582FF9279DOA CRC64;

alignment_scores:
 Quality: 146.00 Length: 88
 Ratio: 2.179 Gaps: 1
 Percent Similarity: 76.136 Percent Identity: 31.818

alignment_block:

US-09-806-382a-1 x 093395 ..

Align seg 1/1 to: 093395 from: 1 to: 101

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1 ATGTGACGAGCTGGAGAAAGCCTGGAATCATGACGAGCTACCA 50
|||||.....|.....|.....|.....|.....|.....|
1 MetGlySerGlnLeuGlnSerMetGlnSerLeuIleThrValPheH 17
51 CAAGTACTCCCTGATTAAGGGAATTTCCATGCCGCTCTACAGGAGTAC 100
|.....|.....|.....|.....|.....|.....|
17 sarGtyrAlaAspLysAspLysAspLysAsnThrLeuSerLysLysL 34
101 TGAAGAAATTGCTAGAGACCGAGTGTCTCAGTATATCAGAAAAAG... 147
|||||.....|.....|.....|.....|.....|.....|
34 euLysGlnLeuMetGlnThrGlnLeuAlaSerPheLeuLysSerGlnL 50
148 .....GGTCAGAGCTGTGTTCAAGAGTTGATATCAACACTCA 188
|||||.....|.....|.....|.....|.....|.....|
51 AspProAlaIleAlaIleAspThrIleMetLysAspLeuAspGlnAsnL 67
189 TGGTGCAGATTAACTTCAGAGAGTTCCTCATTTGCTGATTAAGATGG 238
|||||.....|.....|.....|.....|.....|.....|
67 pGlyLysValSerPheGlnGluPheValSerLeuValValGlyLeuSer 84
239 TGGCAGACCCACAAA 252
:::|.....|.....|
84 LeuLacysGln 88

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seq_name: sp_rodent:Q9D3M4

seq_documentation_block:

ID Q9D3M4 BRELIMINARY; PRT; 94 AA.

AC Q9D3M4;

DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE S100 CALCIUM BINDING PROTEIN A1.
 GN S100A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=HEAD;
 RX MEDLINE=21085660; PubMed=1121851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujona N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Winking L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawai J., Koltzski S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 DR EMBL; AK017279; BAB30670.1; -
 DR HSSP; P04631; 1B4C.
 DR MGD; MGI:1338917; S100a1.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001751; S100_CABP.
 DR Pfam; PF01023; S_100; 1.
 DR SMART; SM00054; EFh; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 SQ SEQUENCE 94 AA; 10487 MW; 7C8B817D135C2D15 CRC64;

alignment_scores:
 Quality: 140.00 Length: 94
 Ratio: 2.154 Gaps: 2
 Percent Similarity: 69.149 Percent Identity: 37.234

alignment_block:

US-09-806-382a-1 x Q9D3M4 ..

Align seg 1/1 to: Q9D3M4 from: 1 to: 94

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1 ATGTGACGAGCTGGAGAAAGCCTGGAATCATGACGAGCTACCA 50
|||||.....|.....|.....|.....|.....|.....|
1 MetGlySerGlnLeuGlnSerMetGlnSerLeuIleThrValPheH 17
51 CAAGTACTCCCTGATTAAGGGAATTTCCATGCCGCTCTACAGGAGTAC 100
|.....|.....|.....|.....|.....|.....|
17 salanHisSerGlyLysGlnGlyLysPylsTyLysSerLysLysL 34
101 TGAAGAAATTGCTAGAGACCGAGTGTCTCAGTATATCAG...AAAAAG 147
|||||.....|.....|.....|.....|.....|.....|
34 euLysAspLeuLeuGlnThrGlnLeuSerGlyPheLeuAspValGlnL 50
148 GGTGACAGCTC.....TGGTTCAAGAGCTGATATCAACACTCA 188
|||||.....|.....|.....|.....|.....|.....|
51 AspAlaAspAlaValAspLysValIleLysGlnLeuAspLysnGlnL 67
189 TGGTGCAGATTAACTTCAGAGAGTTCCTCATTTGCTGATTAAGATGG 238
|||||.....|.....|.....|.....|.....|.....|

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67 pglgluValAspPheylsGluTyrlValValLeuValAlaAlaLeuThrV 84
239 TGGCAGCCACAAAAAGCCATGAAGAAGC 270
|||||:|||||
84 aAlAcysAsnAsnPhetrlpGluThrSer 94

seq_name: sp_rodent:Q91V77

seq_documentation_block:
ID Q91V77 PRELIMINARY; PRT; 94 AA.
AC Q91V77:
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DE 11 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:2700088D09, FULL INSERT SEQUENCE (S100 CALCIUM BINDING PROTEIN
DE A1) (ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610031F03, FULL INSERT SEQUENCE).
GN S100A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arai K., Arai T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara K., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imetani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Kono H., Koyu M., Koyu S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tanigawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=9279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=2049374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format

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RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RA Strusberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Du X.-J., Cole T.J., Tennis N., Gao X.-M., Kontgen F., Kemp B.E.,
RA Heierhorst J.;
RT "Impaired cardiac contractility without cardiomyopathy in S100A1-
RT deficient mice.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK012578; BAB28330.1; -
DR EMBL; BC005590; AAH05590.1; -
DR EMBL; AF368423; AAL14436.1; -
DR EMBL; AK002721; BAB23308.1; -
SQ SEQUENCE 94 AA; 10505 MW; 7C8B817BBF36ED15 CRC64;

alignment_scores:
Quality: 140.00 Length: 94
Ratio: 2.154 Gaps: 2
Percent Similarity: 69.149 Percent Identity: 37.234

alignment_block:
US-09-806-382A-1 x Q91V77 ..
Align seg 1/1 to: Q91V77 from: 1 to: 94

1 ATGTGACCGAGCTCGAGAAAGCCTTGACTCATCATGCAGCTCAGCA 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetGluSerGluLeuGluGlnSerAlaMetGluThrLeuLeuAlaValPheH 17
51 CAGTACTCCCTGATAAGGAGGATTCATGCCGCTCAGAGATGAGC 100
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 SAlaHISerGluGluGlnSerAlaMetGluThrLeuLeuAlaValPheH 34
101 TGAAGAAATGCTAGAGACGAGTCTCCTCAGTATATCAG...AAAAG 147
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 eulysAspLeuLeuGlnThrGluLeuSerGlyPheLeuAspValGlnlys 50
148 GGTGCAAGCTC.....TGGTCAAGAGTTGGATATCAACACTCA 188
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 AspAlaAspAlaValAspLysValMetLysGluLeuAspLysnGlnlys 67
189 TGGTGCAGTTAAGTCCAGAGAGTTCATTCGTGATTAAGATGAGCG 238
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 pglgluValAspPheylsGluTyrlValValLeuValAlaAlaLeuThrV 84
239 TGGCAGCCACAAAAAGCCATGAAGAAGC 270
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 aAlAcysAsnAsnPhetrlpGluThrSer 94

seq_name: sp_human:Q9UCJ0

seq_documentation_block:
ID Q9UCJ0 PRELIMINARY; PRT; 27 AA.
AC Q9UCJ0:
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, last sequence update)
DE CALPROTECTIN LIL SUBUNIT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93139333; PubMed=8423249;
RA Miyasaki K.T., Bodeau A.L., Murthy A.R., Lehrer R.I.;
RT "In vitro antimicrobial activity of the human neutrophil cytosolic S-

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RT 100 protein complex, calprotectin, against Capnocytophaga sputigena."
 RL J. Dent. Res. 72:517-523(1993).
 SO SEQUENCE 27 AA: 3178 MW: BC5E928BEC805CE8 CRC64;

alignment_scores:

Quality: 139.00 Length: 27
 Ratio: 5.148 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382A-1 x Q9UCJ0 ..

Align seg 1/1 to: Q9UCJ0 from: 1 to: 27

```

1  ANGTGACCGAGCTGGAGAAACCTTGAACTGTATCATCGAGCTACCA 50
  |||
1  MetLeuThrGluLeuGluAlaLeuAsnSerIleIleAspValThr 17
51 CAAGTACTCCCTGATTAAGGGAATTTCCAT 81
  |||
17 slystYrSerLeuIleLysGlyAsnPhen 27

```

seq_name: sp_rodent:Q925T3

seq_documentation_block:

ID Q925T3 PRELIMINARY; PRT; 92 AA.

AC Q925T3;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE S100B.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuge O., Yamakawa Y., Nishijima M.;
 RT "Enhancement of transport-dependent decarboxylation of
 RT phosphatidylserine by S100B protein in permeabilized Chinese hamster
 RT ovary cells.";
 RL J. Biol. Chem. 0:0-0(2001).
 DR EMBL: AB056121; BAB43945.1;
 SO SEQUENCE 92 AA: 10749 MW: AF50107EC2BEDF6B CRC64;

alignment_scores:

Quality: 139.00 Length: 92
 Ratio: 2.106 Gaps: 1
 Percent Similarity: 71.739 Percent Identity: 31.522

alignment_block:

US-09-806-382A-1 x Q925T3 ..

Align seg 1/1 to: Q925T3 from: 1 to: 92

```

4  TTGACCGAGCTGGAGAAACCTTGAACTGTATCATCGAGCTACCA 53
  |||
1  MetSerGluLeuGluAlaMetValAlaLeuIleAspIlePheHis 17
54 GTACCCCTGATTAAGGGAATTTCCATCCCTACAGGGATGACCTGA 103
  |||
17 ntySerGluArgGluGlyAspLysHisLysLysLysSerGluLeu 34
104 AGAATTCCTAGAGACCGAGCTGCTCCTCAGTATATC.....AGG 141
  |||
34 ysgLLeuIleAsnAsnGluLeuSerHisPheLeuGluGluLeuLysGlu 50
142 AAAAAGGTGCAGACGCTGCTTCAAGAAGTTGGATATCAACACGTG 191
  |||
51 GlnGluValAlaAspLysValMetGluThrLeuAspGluAspGlyAsp 67

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192 TGCAGTTACTCCAGAGTTCCTCATTCGNGHATAAGATGGCGGTG 241
  |||
67 yGluCysAspPheGlnGluPheMetAlaPheValSerMetValThr 84

```

242 CAGCCCAACAAAAAGCCATGAAGAA 267

84 lacysHisGluPhePheGlnGlu 92

seq_name: sp_rodent:Q9JL08

seq_documentation_block:

ID Q9JL08 PRELIMINARY; PRT; 79 AA.

AC Q9JL08;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE S100 CALCIUM BINDING PROTEIN A1 (FRAGMENT).
 GN S100A1 OR S100A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kiewitz R., Lyons G.E., Schafer B.W., Heizmann C.W.;
 RT "Transcriptional regulation of S100A1 and expression during mouse
 RT heart development.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.
 DR EMBL: AF218353; AAF32320.1; -.
 DR HSP: P04631; IBA4.
 DR MGD: MGI:1338917; S100A1.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001751; S100_Cabp.
 DR Pfam: PF01023; S_100; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE: PS00303; S100_CABP; 1.
 FT NON TER 79
 SO SEQUENCE 79 AA: 8863 MW: F94EDA3A798615D5 CRC64;

alignment_scores:

Quality: 135.00 Length: 79
 Ratio: 2.368 Gaps: 2
 Percent Similarity: 72.152 Percent Identity: 39.241

alignment_block:

US-09-806-382A-1 x Q9JL08 ..

Align seg 1/1 to: Q9JL08 from: 1 to: 79

```

1  ANGTGACCGAGCTGGAGAAACCTTGAACTGTATCATCGAGCTACCA 50
  |||
1  MetGlySerGluLeuGluSerAlaMetGluThrLeuIleAsnValPhe 17
51 CAAGTACTCCCTGATTAAGGGAATTTCCATCCCTACAGGGATGAC 100
  |||
17 salahisSerAlaGlnGluGlyAspLysThrLysLeuSerLysGlu 34
101 TGAAGAAATTCCTAGAGACCGAGCTGCTCCTCAGTATATCAGG...AAAAG 147
  |||
34 eulYAspLeuLeuGlnThrGluLeuSerGlyPheLeuAspValGlnLys 50
148 GGTGCAGAGCTC.....TGCTTCAAGAAGTTGGATATCAACACTGA 188
  |||
51 AspAlaAspAlaValAspLysValMetLysGluLeuAspGluAsnGlyAs 67
189 TCGTCAGTTACTCCAGAGCTCCTCATTCGTGTG 225
  |||
67 pGlyGluValAlaAspPheLysGluThrValValLeuVal 79

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seq_name: sp_mammal:Q9TV56

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seq_documentation_block:
ID Q9TV56 PRELIMINARY; PRT; 101 AA.
AC Q9TV56;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE METASTASIN.
GN MTS1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eumetaria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-MADIN-DURBY; TISSUE-MADIN DARY CANINE KIDNEY (MDCK);
RA Miyamoto H., Hasegawa K., Kim K., Sato H.;
RT "Expression of metastasis associated mts1 gene is co-induced with
RT membrane type-1 matrix metalloproteinase (MT1-MMP) during oncogenic
RT transformation and tubular formation of madin dary canine kidney
RT (MDCK) epithelial cells."
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL: AB031064; BAA83419.1; -.
DR HSP: P30801; 1A03.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_Cabp.
DR Pfam: PF00036; efhand; 1.
DR Pfam: PF01023; S_100; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE: PS00303; S100_CABP; 1.
KW Calcium-binding.
SQ SEQUENCE 101 AA; 11847 MW; 5535387DB7577DF0 CRC64;

alignment_scores:
Quality: 127.00 Length: 79
Ratio: 2.352 Gaps: 1
Percent Similarity: 68.354 Percent Identity: 35.443

alignment_block:
US-09-806-382a-1 x Q9TV56 ..
Align seg 1/1 to: Q9TV56 from: 1 to: 101

1 ATGTTGACGAGCTGGAGAAGCCTGAACCTATCATCATGACGTCATACCA 50
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MetThrPheProLeuGluLysAlaLeuAspValMetValSerThrPheH 17
51 CAAGTACTCCCTGATTAAGGGGAAATTCATGCCGCTACAGGAGATGACC 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 slvstYrSerGlyLysGluLysPheLysLeuAsnArgSerGluL 34
101 TGAAGAAATTTGTAAGACGAGTGTCTCAGATATTCAGAGAAAGGT 150
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 euLysLeuLeuMetArgGluLeuProSerPheLeuGlyLysArgThr 50
151 GCAGAGCTGTGTTCAAGAG.....TTGATATCAACACTGA 188
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 AspGluAlaAlaPheGlnLysLeuMetSerAsnLeuAspSerAsnArgAs 67
189 TGGTGCAGTTAACTTCAGAGAGTTCCTCATTTCTGTGTG 225
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 pasngluValAspPheGlnLutLysValPheLeu 79

seq_name: sp_human:Q9UBG3

seq_documentation_block:
ID Q9UBG3 PRELIMINARY; PRT; 495 AA.
AC Q9UBG3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

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DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TUMOR RELATED PROTEIN.
DE DRCL OR PDRL.
GN DRCL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eumetaria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Xu Z.X., Wang M.R., Cai Y., Xu X., Han Y.L., Wang X.Q., Wu M.;
RT "Cloning and characterization of a novel gene associated with human
RT cancer."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Xu Z.X., Wang M.R., Cai Y., Xu X., Han Y.L., Wang X.Q., Wu M.;
RT "Cloning and characterization of a novel CDNA associated with human
RT cancer."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL: AF07831; AAD55747.1; -.
DR HSP: P02633; 3ICB.
DR InterPro: IPR002046; EF-hand.
DR InterPro: IPR001751; S100_Cabp.
DR Pfam: PF00036; efhand; 1.
DR Pfam: PF01023; S_100; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
KW Calcium-binding.
SQ SEQUENCE 495 AA; 53533 MW; C4882A11B4E64DC3 CRC64;

alignment_scores:
Quality: 126.00 Length: 93
Ratio: 2.032 Gaps: 1
Percent Similarity: 66.667 Percent Identity: 34.409

alignment_block:
US-09-806-382a-1 x Q9UBG3 ..
Align seg 1/1 to: Q9UBG3 from: 1 to: 495

4 TTGACGAGCTGGAGAAGCCTGAACCTATCATCATGACGTCATACCA 53
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MetProGlnLeuGlnAsnIleAsnGlyIleIleGluAlaPheArgAr 17
54 GTACGCCCTGATTAAGGGGAAATTCATGCCGCTACAGGAGATGACCTGA 103
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 gtyrAlaArgThrGluGlyAsnCysThrAlaLeuThrArgGlyGluLeuL 34
104 AGAATTTGTAAGACGAGTGTCTCAGATATTCAGAGAA..... 144
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 ysArgLeuLeuGlnGlnGluPheAlaAspValIleValLysProHisAsp 50
145 ..AAGGTCGACAGCTGTGTTCAAGAGTTCAGATATTCACACTGATGG 191
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 ProAlaThrValAspGluValLeuArgLeuLeuAspGluAspHisThrG 67
192 TGCAGTTAACTTCAGAGAGTTCCTCATTTCTGTGATTAAGATGGCGCTG 241
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 yThrValGluPheLysGluPheLeuValLeuValPheLysValAlaGlnA 84
242 CAGCCACAAAAAGCCATGAGAAAGC 270
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 lacysPheLysThrLeuSerGluSerAla 93

seq_name: sp_human:Q9NTW0

seq_documentation_block:
ID Q9NTW0 PRELIMINARY; PRT; 114 AA.
AC Q9NTW0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)

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DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE MIGRATION INHIBITOR FACTOR-RELATED PROTEIN 14 VARIANT E.
GN S100A9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang M., Xu X., Cai Y., Xu H., Han Y., Xu Z., Wu M.;
RT "Human gene for migration inhibitory factor-related protein 14
RT (MRP14), variant allele."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; AF237582; AAF62537.1; -.
DR HSSP; P02638; ICFP.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_Cabp.
DR Pfam; PF01023; S_100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
SO SEQUENCE 114 AA; 13261 MW; D701528635F4DBC2 CRC64;

alignment_scores:
Quality: 125.50 Length: 92
Ratio: 1.902 Gaps: 1
Percent Similarity: 71.739 Percent Identity: 26.087

alignment_block:
US-09-806-382a-1 x Q9NWM0 ..

Align seg 1/1 to: Q9NWM0 from: 1 to: 114

```
4 TTGACCGAGCTGGAGAAAGCCTTGAACCTATCATGAGCTACACCAA 53
   |||||
5 MetSerGlnLeuGlnArgAsnIleGluThrIleAsnThrPheArgI 21
   |||||
54 GATCTCCCTGATTAAGGGGAATTCATCCCGCTACAGGAGTACTGA 103
   |||||
21 ntyrIerValIlysLeuGlyHisProAspThrLeuAsnGlnGlyI 38
   |||||
104 AGAAATTGCTAGAGACCGAGTGTCTCATATATCAGAAA..... 144
   |||||
38 ysgIleuValArgLysAspLeuGlnAsnPheLeuLysGluAsnLys 54
   |||||
145 .....AAGGGTCAGAGCTGTGGTCAAAAGATTGGATATCAACACTGA 188
   |||||
55 AasnGluLysValIleGluHisIleMetGluAspLeuAspThrAsnAlaAs 71
   |||||
189 TGGTGCACTTAACCTCCAGAGAGTCTCATTTGGTGGTGAATAAGATGGCG 238
   |||||
71 pIysGlnLeuSerPheGlnGluPheIleMetLeuMetAlaArgLeuThr 88
   |||||
239 TGGCAGCCCAACAAAAAGCAGTGA 264
   |||||
88 rPalSerHisGlnLysMetHisGlu 96
```

seq_name: sp_human:Q9UCM6

seq_documentation_block:
ID Q9UCM6 PRELIMINARY; PRT; 25 AA.

AC Q9UCM6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, last annotation update)
DE CALCIUM-BINDING MYELOID RELATED PROTEIN MRP-8 HOMOLOG (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]

RP SEQUENCE.
RX MEDLINE=92406885; PubMed=1326551;
RA Lemarchand P., Vaglio M., Manuel J., Markert M.;
RT "Translocation of a small cytosolic calcium-binding protein (MRP-8) to
RT plasma membrane correlates with human neutrophil activation."
RL J. Biol. Chem. 267:19379-19382(1992).
SO SEQUENCE 25 AA; 2893 MW; 028BEC805CE88619 CRC64;

alignment_scores:
Quality: 125.00 Length: 25
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382a-1 x Q9UCM6 ..

Align seg 1/1 to: Q9UCM6 from: 1 to: 25

```
1 ATGTGACCGAGCTGGAGAAAGCCTTGAACCTATCATGAGCTACCA 50
   |||||
1 MetLeuThrGluLeuGluLysAlaLeuAsnSerIleIleAspValTyrH 17
   |||||
51 CAAGTACTCCCTGATTAAGGGGAAT 75
   |||||
17 slsYrSerLeuIleLysGlyAsn 25
```

seq_name: sp_human:Q9H4U1

seq_documentation_block:
ID Q9H4U1 PRELIMINARY; PRT; 213 AA.

AC Q9H4U1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE DJ14N1.2 (NOVEL S-100/ICABP TYPE CALCIUM BINDING DOMAIN PROTEIN,
DE SIMILAR TO TRICHOHYALIN) (FRAGMENT).
GN DJ14N1.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; AL356504; CAC13173.1; -.
DR HSSP; P02638; ICFP.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001751; S100_Cabp.
DR Pfam; PF01023; S_100; 1.
DR SMART; SM00054; EFh; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 213
SO SEQUENCE 213 AA; 24340 MW; B8C6E0810098E7D2 CRC64;

alignment_scores:
Quality: 122.00 Length: 107
Ratio: 1.848 Gaps: 2
Percent Similarity: 61.682 Percent Identity: 27.103

alignment_block:
US-09-806-382a-1 x Q9H4U1 ..

Align seg 1/1 to: Q9H4U1 from: 1 to: 213

```
4 TTGACCGAGCTGGAGAAAGCCTTGAACCTATCATGAGCTACACCAA 53
   |||||
1 MetThrAspLeuLysSerValIleThrValIleAspValPheTyrLys 17
   |||||
54 GATCTCCCTGATTAAGGGGAATTCATCCCGCTACAGGAGTACTGA 103
```



```

|||||: |||||: |||||: |||||: |||||:
17 STYThrIysGlnAspGlyGlyCysGlyThrLeuSerLysGlyGluLeuL 34
104 AGAAATTCCTAGAGACCGAGTCTCCTAGATATATCAGAAAAAGGT... 150
34 YSGluLeuLeuGluGlyGluLeuHisProValLeuLysAsnProAspAsp 50
151 .....GCAGACGTCTGGTTCAGAAAGTGGATTCACACACTGATGG 191
51 ProAspThrValAspValIleMetHisMetLeuAspArgAspHisAspAr 67
192 TGCAGTTAACTCCAGAGTCCCTCCTGATTCGGTATTAACATGGCGCTG 241
67 GArgLeuAspPheThrGluPheLeuLeuMetIlePheLysLeuThrMetA 84
242 CAGCCACACAAA.....AAA 255
84 lacysAsnLysValLeuSerLysGlyThrCysLysAlaSerGlySerLys 100
256 AGCATTAGAAAGCCACAAA 276
101 LysHisArgArgGlyHisArg 107

```

seq_name: sp_human:Q9B083

```

seq_documentation_block:
ID Q9B083 PRELIMINARY; PRT; 98 AA.
AC Q9B083;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE S100 CALCIUM-BINDING PROTEIN A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY, ADENOCARCINOMA;
RA Strusberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; BC002829; AA02829.1; -.
DR HSSP; P30801; IAO3.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001751; S100_CABP.
DR Pfam; PF01023; S_100; 1.
DR SMART; SM00054; EFh; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 98 AA; 1117 MW; 56D09548450142A9 CRC64;

```

alignment_scores:

Quality:	118.50	Length:	85
Ratio:	2.194	Gaps:	2
Percent Similarity:	63.529	Percent Identity:	34.118

alignment_block:

US-09-806-382A-1 x Q9B083 ..

Align seg 1/1 to: Q9B083 from: 1 to: 98

```

1  AAGTTGACGAGCTGGAAGAGCTTGAACCTATATCAGAGCTCTACCA 50
   ||| :|||:|||||:|||||: |||||: |||||: |||||: |||||:
2  MetCysSerSerLeuGluGlnAlaLeuAlaValLeuValThrPheH 18
51  CAAGTACTCCCTGATTAAGGGAATTTCATCCGCTACAGAGGATGACC 100
   |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||:
18  stysLysSerCysGlnGluGlyAspLysPheLysLeuSerLysGlyLum 35
101 TGAGAGAAATGCTAGAGACGAGTCTCCTCAGATATATCAGAAAAAGGCT 150
   :|||:|||||:|||||: |||||: |||||: |||||: |||||: |||||:

```

```

35 eLysGluLeuLeuHisLysGluLeuProSerPheValGlyLysVal 51
151 GCAGAGCTCTGTTCAAGAG.....TTGCATATTCACACTGA 188
52 AspGluGluGlyLeuLysLysLeuMetGlySerLeuAspGluAsnSerAs 68
189 TGGTGCAGTTAACTCCAGAG.....TTCCCATTCCTGGGATATA 229
68 pGlnGlnValAspPheGlnGluThrAlaValPheLeuAlaLeuIleThrV 85
230 AGATG 234
85 alMet 86

```

seq_name: sp_human:Q01720

```

seq_documentation_block:
ID Q01720 PRELIMINARY; PRT; 591 AA.
AC Q01720;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE FILAGGRIN PRECURSOR (PROFILAGGRIN) (FRAGMENT).
GN Fig.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE=93054736; PubMed=1429717;
RA Presland R.B., Haydock P.V., Fleckman P., Mirnauksiri W., Dale B.A.;
RT "Characterization of the human epidermal profilaggrin gene, genomic
RT organization and identification of an S-100-like calcium binding
RT domain at the amino terminus.";
RL J. Biol. Chem. 267:23772-23781(1992).
CC -1- FUNCTION: AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND PROMOTES
CC DISULFID-BOND FORMATION AMONGST THE INTERMEDIATE FILAMENTS DURING
CC TERMINAL DIFFERENTIATION OF MAMMALIAN EPIDERMIS.
CC -1- PTM: FILAGGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE,
CC HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF
CC 324 AA. THE PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES.
CC DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &
CC PROTEOLYTICALLY CLEAVED.
CC -1- POLYMORPHISM: A NUMBER OF PROFILAGGRIN ISOFORMS HAVE BEEN FOUND
CC WHICH DIFFER BOTH IN SEQUENCE AND IN THE NUMBER OF FILAGGRIN
CC REPEATS.
DR EMBL; L01089; AAA60177.1; -.
DR EMBL; L01090; AAA60176.1; -.
DR HSSP; P02593; ICDM.
DR MIM; 135940; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR003303; Filaggrin.
DR InterPro: IPR001751; S100_CABP.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR PRINTS; PR00487; FILAGGRIN.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Polymorphism.
FT PROPEP 1 293
FT CHAIN 294 467 POTENTIAL.
FT PROPEP 468 474 POTENTIAL.
FT CHAIN 475 >591 POTENTIAL.
FT CA_BIND 19 32 FILAGGRIN.
FT CA_BIND 62 73 SITE I (BY SIMILARITY).
FT NON_TER 591 591 SITE II (BY SIMILARITY).
SQ SEQUENCE 591 AA; 66366 MW; 381491625C75E369 CRC64;

```

alignment_scores:

Quality:	114.50	Length:	113
----------	--------	---------	-----

Ratio: 1.684 Gaps: 4
Percent Similarity: 60.177 Percent Identity: 28.319

alignment_block:

US-09-806-382A-1 x Q01720 ..

Align seg 1/1 to: Q01720 from: 1 to: 591

```

1 ATGTTGACCGAGCTGGAGAAAGCCCTTGAACTCTATCATCGAGCTGTACCA 50
  ||| ||| |||||: : : : : |||||: : : : :
1 MetSerThrLeuLeuGluAsn...IlePheAlaIleIleAsnLeuPheLys 16
51 CAAGTACTCCCTGATTAAGGGGAATTTCCATGCCGCTACAGAGGATGACC 100
  : : ||||| ||| : : : : : : : : :
16 sGlnTyrSerLysLysAspLysAsnThrAspThrLeuSerLysGluL 33
101 TGAAGAAATTCCTAGACAGCCAGTGTCTCAGTATATCAGGAAAAAGGT 150
  |||||: : ||||| ||| ||| : : : : :
33 euLysGluLeuLeuGluLysGluPheArgGlnIleLeuLysAsnProasp 49
151 .....GCAGACGCTGTGTTCAAAGAGTTGGATATCAACACTGA 188
  : : |||||: : : : : : : : : : :
50 AspProAspMetValAspValPheMetAspHisLeuAspIleAspHisAs 66
189 TGGTGCAGTTACTTCAGAGAGTTCCTCATCTGGTATTAAGATGGC. 237
  : : : : : ||||| |||||: : : : : : : : :
66 nLysLysIleAspPheThrGluPheLeuLeuMetValPheLysLeuAlaG 83
238 .....GTGGCAGCCCCAC 249
  : : : : : ||||| : : : : :
83 InAlaTyrTyrGluSerThrArgLysGluAsnLeuProIleSerGlnHis 99
250 .....AAAAAAGCCATGAGAAAGCCCAAGAG 279
  ||| |||||: : : : : : : : :
100 LysHisArgLysHisSerHisAspLysHisGluAsp 112

```

seq_name: sp_human:Q9H4U2

seq_documentation_block:

```

ID Q9H4U2 PRELIMINARY; PRT; 687 AA.
AC Q9H4U2;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE D314N1.1.1 (PROTFLAGGRIN 5' END) (FRAGMENT).
GN FLAG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR EMBL; AL356504; CAC13172.1; -.
DR HSSP; P02593; ICDM.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR003303; Filaggrin.
DR Pfam; PF01023; S_100; 1.
DR PRINTS; PR00487; FLAGGRIN.
DR SMART; SM00054; EFh; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 687
SQ SEQUENCE 687 AA; 76659 MW; 8000363FBEF07B74 CRC64;

```

alignment_scores:

Quality: 114.50 Length: 113
Ratio: 1.684 Gaps: 4
Percent Similarity: 60.177 Percent Identity: 28.319

alignment_block:

US-09-806-382A-1 x Q9H4U2 ..

Align seg 1/1 to: Q9H4U2 from: 1 to: 687

```

1 ATGTTGACCGAGCTGGAGAAAGCCCTTGAACTCTATCATCGAGCTGTACCA 50
  ||| ||| |||||: : : : : |||||: : : : :
1 MetSerThrLeuLeuGluAsn...IlePheAlaIleIleAsnLeuPheLys 16
51 CAAGTACTCCCTGATTAAGGGGAATTTCCATGCCGCTACAGAGGATGACC 100
  : : ||||| ||| : : : : : : : : :
16 sGlnTyrSerLysLysAspLysAsnThrAspThrLeuSerLysGluL 33
101 TGAAGAAATTCCTAGACAGCCAGTGTCTCAGTATATCAGGAAAAAGGT 150
  |||||: : ||||| ||| ||| : : : : :
33 euLysGluLeuLeuGluLysGluPheArgGlnIleLeuLysAsnProasp 49
151 .....GCAGACGCTGTGTTCAAAGAGTTGGATATCAACACTGA 188
  : : |||||: : : : : : : : : : :
50 AspProAspMetValAspValPheMetAspHisLeuAspIleAspHisAs 66
189 TGGTGCAGTTACTTCAGAGAGTTCCTCATCTGGTATTAAGATGGC. 237
  : : : : : ||||| |||||: : : : : : : : :
66 nLysLysIleAspPheThrGluPheLeuLeuMetValPheLysLeuAlaG 83
238 .....GTGGCAGCCCCAC 249
  : : : : : ||||| : : : : :
83 InAlaTyrTyrGluSerThrArgLysGluAsnLeuProIleSerGlnHis 99
250 .....AAAAAAGCCATGAGAAAGCCCAAGAG 279
  ||| |||||: : : : : : : : :
100 LysHisArgLysHisSerHisAspLysHisGluAsp 112

```

OM of: US-09-806-382A-1 to: A_Geneseq_032802: * out_format : pfs
Date: Sep 9, 2002 3:10 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

```
-MODEL=frame_m2p.model -DEV=xlp  
-Q=/cgn2_1/USPTO_pool/US09806382/runat_09092002_143847_15354/app_query.fasta_1.752  
-DB=A_Geneseq_032802 -QFMT=fastan -SUFFIX=rag -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELCP=6.000 -DELEXT=7.000 -START=1 -MATRIX=biosum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09806382 @CGNL_1_120 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPRX -WAIT -THREADS=1
```

Search information block:

```
Query: US-09-806-382A-1  
Query length: 282  
Database: A_Geneseq_032802: *  
Database sequences: 747574  
Database length: 11107396  
Search time (sec): 103.790000
```

Score_list:

Sequence	Strd Orig	ZScore	EScore	Len	! Documentation
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:AAW17061			485.00	1192.05	3.2e-58
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW60177			485.00	1192.05	3.2e-58
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW45538			485.00	1192.05	3.2e-58
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW87635			485.00	1192.05	3.2e-58
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW44595			485.00	1192.05	3.2e-58
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW31906			485.00	1192.05	3.2e-58
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW31910			485.00	1192.05	3.2e-58
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW78376			485.00	1192.05	3.2e-58
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW79360			426.00	1038.52	6.0e-35
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:AAW50052			317.00	778.16	2.2e-35
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:AAW24299			295.00	720.33	6.4e-32
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:AAW45436			160.00	384.48	3.1e-13
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:AAW03564			158.00	379.51	6.0e-13
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:AAW24137			158.00	379.51	6.0e-13
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW45542			158.00	379.51	6.0e-13
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW31907			158.00	379.51	6.0e-13
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW31908			158.00	379.51	6.0e-13
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW31911			156.00	374.65	1.1e-12
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW31909			154.00	369.23	2.2e-12
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW45545			154.00	369.23	2.2e-12
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW40258			154.00	367.40	2.3e-12
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW90764			153.00	367.32	2.9e-12
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW90765			153.00	367.32	2.9e-12
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW01826			151.00	362.23	5.5e-12
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:AAW93819			145.00	346.98	3.8e-11
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW45531			145.00	346.98	3.8e-11
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW40258			135.00	322.01	9.2e-10
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW27582			134.00	322.16	1.2e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW601409			134.00	317.51	1.4e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW31903			133.50	316.36	1.6e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:AAW17062			133.50	316.36	1.6e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW60178			133.50	316.36	1.6e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:AAW45615			133.50	316.36	1.6e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW45539			133.50	316.36	1.6e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAW87637			133.50	316.36	1.6e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW44613			133.50	316.36	1.6e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW31905			133.50	316.36	1.6e-09
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW35994			133.50	313.33	1.8e-09

/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW46607 + 133.00 317.49. 1.7e
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW44612 + 131.50 311.48 3.0e
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAW6133 + 130.00 310.04 4.5e
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:AAW20560 + 126.00 299.00 1.7e
/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:AAW80453 + 126.00 299.00 1.7e

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:AAW17061

seq_documentation_block:

ID AAW17061 standard; Protein; 93 AA.

AC AAW17061;

DT 16-JUL-1997 (first entry)

DE Human multidrug resistance protein 8 (MRP8).

KW Genetic engineering; MRP; multidrug resistance protein; transgenic;

KW animal model; cell death inhibition; apoptosis; cell proliferation;

KW HIV; human immunodeficiency virus; cancer; cystic fibrosis; neoplasia.

OS Homo sapiens.

PN US5614397-A.

PD 25-MAR-1997.

PR 22-FEB-1994; 94US-0200016.

PR 22-FEB-1994; 94US-0200016.

PA (STRD) UNIV LEIAND STANFORD JUNIOR.

PI Lagasse E, Weissman I;

DR WPI: 1997-224943/20.

XX N-FSDB; AAT68321.

PT Increasing life-span of mammalian haemato-lymphoid cells by

transferring stem cells - with construct contg. cell-specific

transcription initiator and gene encoding protein that increases

lifetime, useful for drug screening and treatment

PS Example 1; Column 27-28; 34pp: English.

XX AAW17061 is the human MRP8 protein. The transcriptional initiator of the

MRP8 gene was used in a construct for expressing an open reading frame

that increase the lifespan of a mammalian haematolymphoid cell, e.g. the

mammalian bcl-2 gene, a CTR (cystic fibrosis transmembrane regulator)

gene, the herpes virus thymidine kinase gene or an oncogene.

CC Haematolymphoid cells are especially neutrophils and the construct

doubles the lifespan of transgenic cells. Transgenic cells or

transgenic animals produced are used for screening for substances and

treatments that prevent or promote cell death. They can also be returned

to the patient to modulate apoptosis, i.e. in the treatment of disorders

related to abnormal cell proliferation or death. Typical applications

are treatment of viral diseases, including HIV; cancer and cystic

XX fibrosis.

Sequence 93 AA;

alignment_scores:

Quality: 485.00

Ratio: 5.215

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

US-09-806-382A-1 x AAW17061 ..

Align seg 1/1 to: AAW17061 from: 1 to: 93

1 AMGTGACGAGCTGAGAAAGCCCTTACATCATGACGCTCTACCA 50

PI Katus HA, Remppis A;
XX
XX MPI: 2000-673510/66.
DR N-PSDB; AAC81808.
XX

PT Composition containing S100 protein, corresponding nucleic acid or
PT vector, useful for treating cardiomyopathy and cardiac insufficiency
XX

PS Claim 35; Page 15; 36pp; German.

XX This invention describes a novel composition for treating primary or
XX secondary cardiomyopathy or cardiac insufficiency contains at least one
XX S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
XX fragments, or a gene transfer vector containing (II), optionally
XX formulated with auxiliaries and/or carriers. (I) are calcium-binding
XX proteins involved in calcium homeostasis, so their overexpression in
XX cardiac muscle will improve pumping capacity (and overall capacity) of
XX the heart. In cultured myocardial cells they increase the contraction and
XX relaxation rates associated with increased systolic calcium ion release
XX from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
XX used to treat cardiomyopathy (CMP) where inherited or caused by
XX spontaneous mutations and ischemic CMP caused by arteriosclerosis,
XX dilative CMP caused by toxic/infectious disease, cardiac disease caused
XX by pulmonary and/or arterial hypertension, and structural disease caused
XX by rhythm disorders or valve defects, generally any condition associated
XX with reduced contractile force. Unlike calmodulin, which is expressed
XX ubiquitously, (I) show tissue-specific expression and treat the
XX underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
XX disease.

XX Sequence 93 AA;
SQ

alignment_scores: Quality: 485.00 Length: 93
 Ratio: 5.215 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382a-1 x AAB45538 ..

Align seg 1/1 to: AAB45538 from: 1 to: 93

```
1  ATGTTGACCGAGCTGGAGAAAGCCTTGAACCTATATCATGAGCGTTACCA 50
|||||
1  MetLeuThrGluLeuGluAlaLeuAsnSerIleIleSprValTyrHn 17
51  CAAGTACTCCCTGATAAAGGGGAATTTCATGCCGTCTACAGGGATGACC 100
|||||
17  slvstySerLeuIleLysGluYasnPhenIleAlaValTyrArgAspAspRL 34
101 TGAAGAAATGCTAGAGACCGAGTGTCTCAGTATATCAGGAAAAAGGCT 150
|||||
34  euLysLysLeuLeuGluThrGluCysProGlnTyrIleArgLysGly 50
151 GCAGAGCTCTGTTCAAGAGTTGATATCAACATGATGCTGCTACCTAA 200
|||||
51  AlaAspValIleThrPheLysGluLeuAspIleAsnThrAspGluAlaValAs 67
201 CTTCACGAGAGTTCTCATCTGTGGTGAATAAGATGGCGGTGACGCCACA 250
|||||
67  nPheGlnGluThrPheLeuIleLeuValIleLysMetGlyValAlaIleHnIle 84
```

251 AAAAAAGCCATGAAAGAAAGCCACAAGAG 279

84 yLysSerHnIsgLysGluSerHnIsgLysGlu 93

seq_name: /SIDS1/ycgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT: AAY87636

seq_documentation_block:

ID AAY87636 standard; Protein: 93 AA.

XX
AC AAY87636;

XX 04-AUG-2000 (first entry)
DT
XX
DE Human calcium-binding protein #1.
XX

KW Calcium-binding protein; granule release; calgranulin; human;
KW vascular membrane growth; adult respiratory distress syndrome;
KW acute myocardial infarction; ischemic reperfusion disorder;
KW glomerulonephritis; rheumatoid arthritis; chronic bronchitis;
KW cerebral vascular disorder; asthma; peripheral circulation disturbance;
KW angina pectoris; hypertension; multiple sclerosis.
XX

OS Homo sapiens.

PN W0200018970-A1.

PD 06-APR-2000.

PF 28-SEP-1999; 99WO-JP05302.

PR 29-SEP-1998; 98JP-0274574.

PA (ASAH) ASAH KASEI KOGYO KK.

PI Seto M, Fukuda K;

XX MPI: 2000-293189/25.

DR N-PSDB; AAA11969.

XX

PT

PS

XX

Controlling the release of granules from cell system using activated
calgranulin for screening substances for granule activating or
inhibiting activity -
Disclosure; Page 37-38; 42pp; Japanese.

This invention describes a novel method for controlling the release of
granules by treating a cell system to increase or decrease activated
calgranulin to enhance or depress the release of granules. Calgranulin
is a calcium binding protein and can be used for controlling the release
of granules from a cell system e.g. those involved with the inhibition of
vascular membrane growth. Vascular membrane growth is associated with
e.g. adult respiratory distress syndrome, acute myocardial infarction due
to ischemic reperfusion disorders, glomerulonephritis, rheumatoid
arthritis, chronic bronchitis, cerebral vascular disorders, asthma,
peripheral circulation disturbance, angina pectoris, hypertension and
multiple sclerosis. The new method is used for screening substances for
their ability to activate or inhibit the release of granules. This
sequence represents a human calcium-binding protein which is described in
the method of the invention.

SQ Sequence 93 AA;

alignment_scores: Quality: 485.00 Length: 93
 Ratio: 5.215 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382a-1 x AAY87636 ..

Align seg 1/1 to: AAY87636 from: 1 to: 93

```
1  ATGTTGACCGAGCTGGAGAAAGCCTTGAACCTATATCATGAGCGTTACCA 50
|||||
1  MetLeuThrGluLeuGluAlaLeuAsnSerIleIleSprValTyrHn 17
51  CAAGTACTCCCTGATAAAGGGGAATTTCATGCCGTCTACAGGGATGACC 100
|||||
17  slvstySerLeuIleLysGluYasnPhenIleAlaValTyrArgAspAspRL 34
101 TGAAGAAATGCTAGAGACCGAGTGTCTCAGTATATCAGGAAAAAGGCT 150
|||||
```

34 eulysleuLeuGlutHrGlucysProGlnTyrIleArglyslsly 50
151 GCAGAGCTGCTGTTCAAGAGTTGGATATCAACACTGATGTCAGTTAA 200
51 AlaaspvaltrpPheIysGluLeuAspIleAsnThrAspGlyAlaValas 67
201 CTTCCAGAGGATCCCTCATTCCTGATTAAGATGGCCGTCGACGCCACA 250
67 nPheGlnGluPheLeuIleLeuValIleLysMetGlyValAlaIleHisL 84
251 AAAAAAGCCATGAGAACCCACAAAGAG 279
84 yslsSerHisGluGlnSerHisIlysglu 93

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:ABB44595

seq_documentation_block:
ID ABB44595 standard; Protein: 93 AA.

AC ABB44595:

DT 25-JAN-2002 (first entry)

DE Human wound healing related polypeptide SEQ ID NO 54.

KW Human; mouse; vulnery; dermatological; skin disorder; wound healing;
KW gene therapy.

OS Homo sapiens.

PN CA2325226-A1.

PD 17-MAY-2001.

PE 16-NOV-2000; 2000CA-2325226.

PR 17-NOV-1999; 99DE-1055349.

PR 17-DEC-1999; 99US-0172511.

PR 20-JUN-2000; 2000DE-1030149.

PA (SWIT-) SWITCH BIOTECH AG.

PI Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;

DR WPI: 2001-433142/47.

PT Use of novel polypeptide or its variant or nucleic acid encoding the
PT polypeptide for diagnosing and/or preventing and/or treating skin
PT disorders and/or treatment in wound healing or for identifying active
PT substances -

PS Claim 3; Page 220; 265pp; English.

XX The invention relates to the use of a polypeptide (ABB44544-ABB44601,
CC ABB44606-ABB44623) or its variant or encoding nucleic acid
CC (ABA81990-ABA81995, ABA82016-ABA82032) with vulnery and/or
CC dermatological activity for the diagnosis, prevention and treatment of
CC skin disorders and treatment in wound healing or for the identification
CC of pharmacologically active substances. The nucleic acids are useful in
CC gene therapy.

CC Note: The printed sequence listing for this specification was incomplete,
CC terminating part way through SEQ ID NO 106. The remaining data was
CC obtained from EPO data for an equivalent patent (EP1144862).

XX Sequence 93 AA;

alignment_scores:

Quality: 485.00 Length: 93
Ratio: 5.215 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382a-1 x ABB44595 ..

Align seg 1/1 to: ABB44595 from: 1 to: 93

1 ATGTGACCCAGACTGGAGAAAGCTTGAACCTATCATGAGCTACCA 50
1 MetLeuThrGluLeuGluLysAlaLeuAsnSerIleIleAspValIlyrnl 17
51 CAAAGTACTCCCTGATTAAGGGAATTTCCATGCCGCTACAGGAGGAC 100
17 slsYrSerIleuIleLysGlyAsnPhenIleAlaValIlyrArGspAspL 34
101 TGAAGAAATGCTAGAGCCAGTGTCTCAGTATATCAAGAAAGGCT 150
34 eulysleuLeuGlutHrGlucysProGlnTyrIleArglyslsly 50
151 GCAGAGCTGCTGTTCAAGAGTTGGATATCAACACTGATGTCAGTTAA 200
51 AlaaspvaltrpPheIysGluLeuAspIleAsnThrAspGlyAlaValas 67
201 CTTCCAGAGGATCCCTCATTCCTGATTAAGATGGCCGTCGACGCCACA 250
67 nPheGlnGluPheLeuIleLeuValIleLysMetGlyValAlaIleHisL 84
251 AAAAAAGCCATGAGAACCCACAAAGAG 279
84 yslsSerHisGluGlnSerHisIlysglu 93

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:AAB31906

seq_documentation_block:
ID AAB31906 standard; Protein: 93 AA.

AC AAB31906:

DT 15-MAY-2001 (first entry)

DE Amino acid sequence of a human protein.

XX

KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;

KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;

KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;

KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;

KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.

OS Homo sapiens.

PN WO200105422-A2.

PD 25-JAN-2001.

PE 17-JUL-2000; 2000WO-FR02057.

PR 15-JUL-1999; 99FR-0009372.

PA (INNR) BIOMERIEUX STELHYS.

PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;

DR WPI: 2001-159475/16.

PT Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand -

PS Claim 1; Page 166; 209pp; French.

XX The present sequence represents a human protein, which is used in the
XX method of the invention. The specification describes a method which uses
XX at least one polypeptide or polynucleotide sequence belonging to the
XX perlecan, precursor of the retinol-binding plasma protein, precursor of
XX the ganglioside GM2 activator, calgranulin B or saposin B protein
XX families. The method is used for detecting, preventing or treating a

CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms
CC and phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and
CC in gene therapy (expression of sense or antisense sequences). They can
CC also be used to assess efficacy of potential therapeutic agents,
CC particularly compounds that reduce or inhibit toxicity towards glial
CC cells.

SO Sequence 93 AA:

alignment_scores: Length: 93
 Quality: 485.00 Gaps: 0
 Ratio: 5.215
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382a-1 x AAB31906 ..

Align seg 1/1 to: AAB31906 from: 1 to: 93

```
1 ATGTTGACGAGCTGGAGAAAGCCTGAACCTATCATGACGCTTACCA 50
|||||
1 MetLeuThrGluLeuGluAlaLeuAsnSerIleIleAspValTyrH 17
51 CAAGTACTCCCTGATTAAGGGGAATTTCCATGCCGTCTACAGGGATGACC 100
|||||
17 sLysTyrSerLeuIleLysGluAsnPhenAlaValTyrArgAspAsp 34
101 TGAAGAAATTCCTAGAGACCGAGTCTCATATATCAGAAAAAGGT 150
|||||
34 euLysLysLeuLeuGluThrGluCysProGlnTyrIleArgLysGly 50
151 GCAGACGCTGCTTCAAGAGTGGATATCAACATGATGGGCGACCCACA 200
|||||
51 AlaAspValTyrPheLysGluLeuAspIleAsnThrAspGlyAlaValAs 67
201 CTTCAGAGAGTTCCTCATTTCTGTGATTAAGATGGCGTGGCAGCCACA 250
|||||
67 nPheGlnGluPheLeuIleLeuValIleLysMetGlyValAlaIleAsn 84
251 AAAAAGCCATGAAGAAAGCCACAAAGAG 279
|||||
84 yslYsSerHisGluGluSerHisLysGlu 93
```

seq_name: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:AAB31910

seq_documentation_block:

ID AAB31910 standard; Protein: 93 AA.

AC AAB31910;

DT 15-MAY-2001 (first entry)

DE Amino acid sequence of a human protein.

XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KM ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KM neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KM Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KM rheumatoid polyarthritis; lupus erythematosus; gene therapy.

XX Homo sapiens.

OS WO200105422-A2.

PN 25-JAN-2001.

PD 17-JUL-2000; 2000WO-FR02057.

XX

PR 15-JUL-1999; 99FR-0009372.
XX
XX (INMR) BIONERIEUX STELHYS.

PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX WPI; 2001-159475/16.

DR Detecting, preventing and treating degenerative, neurological and
XX autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand

PS Claim 1; Page 168; 209pp; French.

XX The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms
CC and phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and
CC in gene therapy (expression of sense or antisense sequences). They can
CC also be used to assess efficacy of potential therapeutic agents,
CC particularly compounds that reduce or inhibit toxicity towards glial
CC cells.

SO Sequence 93 AA:

alignment_scores: Length: 93
 Quality: 485.00 Gaps: 0
 Ratio: 5.215
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-806-382a-1 x AAB31910 ..

Align seg 1/1 to: AAB31910 from: 1 to: 93

```
1 ATGTTGACGAGCTGGAGAAAGCCTGAACCTATCATGACGCTTACCA 50
|||||
1 MetLeuThrGluLeuGluAlaLeuAsnSerIleIleAspValTyrH 17
51 CAAGTACTCCCTGATTAAGGGGAATTTCCATGCCGTCTACAGGGATGACC 100
|||||
17 sLysTyrSerLeuIleLysGluAsnPhenAlaValTyrArgAspAsp 34
101 TGAAGAAATTCCTAGAGACCGAGTCTCATATATCAGAAAAAGGT 150
|||||
34 euLysLysLeuLeuGluThrGluCysProGlnTyrIleArgLysGly 50
151 GCAGACGCTGCTTCAAGAGTGGATATCAACATGATGGGCGACCCACA 200
|||||
51 AlaAspValTyrPheLysGluLeuAspIleAsnThrAspGlyAlaValAs 67
201 CTTCAGAGAGTTCCTCATTTCTGTGATTAAGATGGCGTGGCAGCCACA 250
|||||
67 nPheGlnGluPheLeuIleLeuValIleLysMetGlyValAlaIleAsn 84
251 AAAAAGCCATGAAGAAAGCCACAAAGAG 279
|||||
84 yslYsSerHisGluGluSerHisLysGlu 93
```

seq_name: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:AAM78376

seq_documentation_block:

ID AAM78376 standard; Protein: 171 AA.

XX

AC AAM78376;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1038.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN MO200157190-A2.
XX
PD 09-AUG-2001.
XX
PE 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HXSE-) HXSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB: AAK51509.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3275-3276; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 171 AA;

alignment_scores:
Quality: 485.00 Length: 93
Ratio: 5.215 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-806-382A-1 x AAM78376 ..

Align seg 1/1 to: AAM78376 from: 1 to: 171

1 ATGTTGACCGAGCTGGAGAAAGCCTTGAACCTCATCATGAGCTCTACCA 50
|||||
79 MetLeuThrGluLeuGlnLysAlaLeuAsnSerIleIleAspValTyrH 95

51 CAAGTACTCCCTGATAAAGGGAATTCACGCGCTCTACAGGATGACC 100
|||||
95 sluyTyrSerIleuIleIleYsGlyAsnPhenHisAlaValTyrArgAspAsp 112
101 TGAAGAAATTCCTAGAGACCGAGCTGCTCAGTATATCAGAGAAAGGCT 150
|||||
112 euIysLysLeuLeuGlnTyrHrGluCySProGlnTyrIleArgLysGly 128
151 GCAGAGCTGCTGTTCAAGAGTTGATATCAACACGTGATGCTGACGTTAA 200
|||||
129 AlaAspValTyrPheLysGluLeuAspIleAsnThrAspLysAlaValAs 145
201 CTTCCAGAGATTCCATTCCTGCTGATAAAGATGGCGCTGACCCACA 250
|||||
145 nrPheGlnGluPheLeuIleLeuValIleLysMetGlyValAlaIleHisL 162
251 AAAAAGCCATGAAAGCCACCAAGAG 279
|||||
162 yslYsSerHisGlnGluSerHisLysGlu 171

seq_name: /SIDSL/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT: AAM79360
seq_documentation_block:
ID AAM79360 standard; Protein: 179 AA.
XX
AC AAM79360;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3006.
XX
PI Human protein SEQ ID NO 3006.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PE 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HXSE-) HXSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB: AAK52493.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 229; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

Sequence 179 AA:

alignment_scores: Length: 92
 Quality: 426.00
 Ratio: 4.897
 Gaps: 0
 Percent Similarity: 94.365 Percent Identity: 91.304

alignment_block:
 US-09-806-382a-1 x AAM79360 ..

Align seg 1/1 to: AAM79360 from: 1 to: 179

```

1  ATGTTGACCGAGCTGGAGAAAGCCTTGAACCTATCATCGACGCTACCA 50
   ||||||||||||||||||||||||||||||||||||||||||||||||
15 MetLeuThrGluLeuGluLysAlaLeuAsnSerIleIleAspValTyrH 31
51 CAAGTACCTCCCTGATTAAGGGGAATTCATGCCGCTCAGAGGATGACC 100
   ||||||||||||||||||||||||||||||||||||||||||||||||
31 slystySerLeuIleLysGlyAsnPhenIleAlaValTyrArgAspAspL 48
101 TGAAGAAATTTGCTAGAGACCGAGTCTCTCAGTATATCAGAAAAAGGT 150
   ||||||||||||||||||||||||||||||||||||||||||||||||
48 euLysLysLeuLeuGluThrGluCysProGlnTyrIleArgLysLysGly 64
151 GCAGACGCTGCTGTTCAAGAGTTGGATATCAACCTGATGGTGCAGTTAA 200
   ||||||||||||||||||||||||||||||||||||||||||||||||
65 AlaAspValTyrPheLysGlyLeuAspIleAsnThrAspGlyAlaValAs 81
201 CTTCACGAGATTCCTCATCTGCTGATTAAGATGGCGTGGCAGCCACCA 250
   ||||||||||||||||||||||||||||||||||||||||||||||||
81 nPheGlnGluPheLeuIleLeuValIleLysMetGlyValAlaIleLeuA 98
251 AAAAAAGCCATGAAGAAAGCCACAAA 276
   ::::: |||||
98 snSerIleIleAspValTyrHisLys 106

```

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:AAp50052

seq_documentation_block:

ID AAP50052 standard; Protein: 66 AA.

AC AAP50052;

DT 09-SEP-1991 (first entry)

DE Sequence of human macrophage migration inhibiting factor (MIF).

KW Autoimmune disease therapy; tumour therapy; leprosy; tuberculosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 42 /label= S,C

XX EPI62812-A.

XX 27-OCT-1985.

XX 15-MAY-1985; 85EP-0810232.

XX 05-FEB-1985; 85CH-0000512.

PR 24-MAY-1984; 84CH-0002557.
 PR 07-AUG-1984; 84CH-0003786.
 PR 14-NOV-1984; 84CH-0005446.
 XX
 PA (CIBA) CIBA GEIGY AG.

XX Sorg C, Burmeister G, Tarcsay L, Wiesendanger W;
 PI WPI; 1985-298143/48.
 DR
 XX

PT Pure human macrophage migration inhibiting factor - specific
 PT monoclonal antibodies and hybridoma cell lines, useful e.g. for
 PT treating auto-immune disease

PS Claim 5; Page 38; 48pp; German.

CC MIF is used for increasing resistance to infection (e.g.
 CC tuberculosis, leprosy, leishmaniasis or candidiasis) and to tumours
 CC (esp. metastases).
 CC
 XX

SO Sequence 66 AA;

alignment_scores: Length: 66
 Quality: 317.00
 Ratio: 5.032
 Gaps: 0
 Percent Similarity: 95.455 Percent Identity: 93.939

alignment_block:
 US-09-806-382a-1 x AAP50052 ..

Align seg 1/1 to: AAP50052 from: 1 to: 66

```

1  ATGTTGACCGAGCTGGAGAAAGCCTTGAACCTATCATCGACGCTACCA 50
   ||||||||||||||||||||||||||||||||||||||||||||||||
1 MetLeuThrGluLeuGluLysAlaLeuAsnSerIleIleAspValTyrH 17
51 CAAGTACCTCCCTGATTAAGGGGAATTCATGCCGCTCAGAGGATGACC 100
   ||||||||||||||||||||||||||||||||||||||||||||||||
17 slystySerLeuIleLysGlyAsnPhenIleAlaValTyrArgAspAspL 34
101 TGAAGAAATTTGCTAGAGACCGAGTCTCTCAGTATATCAGAAAAAGGT 150
   ||||||||||||||||||||||||||||||||||||||||||||||||
34 euLysLysLeuLeuGluThrGlu***ProGlnTyrIleArgLysLysGly 50
151 GCAGACGCTGCTGTTCAAGAGTTGGATATCAACCTGATGGTGCAGTT 198
   ||||||||||||||||||||||||||||||||||||||||||||||||
51 AlaAspValTyrPheLysGlyLeuAspIleAsn*****AlaVal 66

```

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:AAr22429

seq_documentation_block:

ID AAR22429 standard; Protein: 89 AA.

AC AAR22429;

DT 12-AUG-1992 (first entry)

DE Murine CP-10.

KW Chemotactic protein; neutrophil; monocyte; macrophage;
 KW inflammation; autoimmune disease; delayed hypersensitivity;
 KW CF; cystic fibrosis; emphysema; diagnosis.

OS Mus musculus.

XX W09204376-A.

XX 19-MAR-1992.

XX 05-SEP-1991; 91WO-AU00410.

XX 05-FEB-1991; 91AU-0004463.

PR 05-SEP-1990; 90AU-0002127.
XX
XX (HEAR-) HEART RES INST LTD.
XX
PI Geczy C, Simpson RJ, Lackmann M;
XX
XX WPI; 1992-114301/14.
DR N-PSDB; AA023343.
XX
XX New chemotactic protein CP-10 for altering inflammatory capacity
PT - controls inflammatory conditions, cystic fibrosis and
PT emphysema, antagonists for detecting CP-10
XX
XX
PS Claim 3; Page 36; 56pp; English.
XX
XX The mCP10 cDNA was derived from a Sepharose-Concanavalin A-activated
CC spleen cell library prep. using cells from A/J mice. CP-10 has an
CC apparent mol. wt. of ca. 10 kD and is chemotactic for neutrophils,
CC monocytes/macrophages and/or other mammalian cells. CP-10 is useful
CC (e.g. when admin. locally around a tumour or site of infection) to
CC attract neutrophils etc., esp. in immunocompromised patients or
CC patients allergic to skin test antigens. Antibodies to CP-10 are
CC useful for control of inflammation and/or tissue damage associated
CC with inflammation, (e.g. due to autoimmune disease or delayed
CC hypersensitivity), cystic fibrosis or emphysema. Ab can also be used
CC purely CP-10 and in diagnosis.
XX
XX
SQ Sequence 89 AA;

alignment_scores:
Quality: 295.00 Length: 89
Ratio: 3.734 Gaps: 0
Percent Similarity: 88.764 Percent Identity: 58.427

alignment_block:
US-09-806-382A-1 x AAR22429 ..

Align seg 1/1 to: AAR22429 from: 1 to: 89

1 ATGTTGACCGAGCTGAGAAAGCCTTGACCTATCATCGACGCTACCA 50
||| :::
1 MetProserGluLeuGluLysAlaLeuSerAsnLeuIleAspValYrHl 17

51 CAAGTACTCCCTGATTAAGGGAAATTCATGCCGTCACAGGATGACC 100
|:::||||| |:::||||| |:::||||| |:::||||| |:::|||||
17 sAsnTySerAsnIleGlnGlyAsnHisAlaLeuTyLysAsnAsp 34

101 TGAAGAAATTCCTAGACCGAGCTGCTCAGATATACAGAAAGCGT 150
:::|||||::: |:::|||||::: |:::|||||::: |:::|||||:::
34 heLysLysMetValThrThrGluCysProGlnPheValGlnAsnIleAsn 50

151 GCAGACGCTGGTTCAAAGAGTTGGATATACACAGTATGTCAGTTAA 200
::: |:::|||||::: |:::|||||::: |:::|||||::: |:::|||||
51 IleGluAsnLeuPheArgGluLeuAspIleAsnSerAspAsnAlaIleAs 67

201 CTTCAGAGATTCCTCATTCCTGATGAAGAATGGCGCTGGCAGCCACA 250
|:::|||||::: |:::|||||::: |:::|||||::: |:::|||||:::
67 nPheGluGluPheLeuAlaMetValIleLysValGlyValAlaSerHisL 84

251 AAAAAGCCATGAAGA 267
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84 yAspSerHisLysGlu 89

seq_name: /STD1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT: ABB44594

seq_documentation_block:
ID ABB44594 standard; Protein; 89 AA.
XX
AC ABB44594;
XX
XX 25-JAN-2002 (first entry)
XX
XX

DE Mouse wound healing related polypeptide SEQ ID NO 53.
XX
XX Human; mouse; vulnery; dermatological; skin disorder; wound healing;
KW gene therapy.
KW
XX
XX Mus musculus.
OS
XX
XX CA2325226-A1.
PN
XX
XX 17-MAY-2001.
PD
XX
XX 16-NOV-2000; 2000CA-2325226.
PF
XX
XX 17-NOV-1999; 99DE-1055349.
PR 17-DEC-1999; 99US-0172511.
PR 20-JUN-2000; 2000DE-1030149.
XX
XX (SWIT-) SWITCH BIOTECH AG.
PA
XX
XX Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;
PI WPI; 2001-433142/47.
XX
XX
XX Use of novel polypeptide or its variant or nucleic acid encoding the
PT polypeptide for diagnosing and/or preventing and/or treating skin
PT disorders and/or treatment in wound healing or for identifying active
PT substances
XX
XX
PS Disclosure: Page 219-220; 265pp; English.
XX
XX The invention relates to the use of a polypeptide (ABB44544-ABB44601,
CC ABB44606-ABB44623) or its variant or encoding nucleic acid
CC (ABA81990-ABA81995, ABA82016-ABA82032) with vulnery and/or
CC dermatological activity for the diagnosis, prevention and treatment of
CC skin disorders and treatment in wound healing or for the identification
CC of pharmacologically active substances. The nucleic acids are useful in
CC gene therapy.
CC Note: The printed sequence listing for this specification was incomplete,
CC terminating part way through SEQ ID NO 106. The remaining data was
CC obtained from EPO data for an equivalent patent (EP1114862).
XX
XX
SQ Sequence 89 AA;

alignment_scores:
Quality: 295.00 Length: 89
Ratio: 3.734 Gaps: 0
Percent Similarity: 88.764 Percent Identity: 58.427

alignment_block:
US-09-806-382A-1 x ABB44594 ..

Align seg 1/1 to: ABB44594 from: 1 to: 89

1 ATGTTGACCGAGCTGAGAAAGCCTTGACCTATCATCGACGCTACCA 50
||| :::
1 MetProserGluLeuGluLysAlaLeuSerAsnLeuIleAspValYrHl 17

51 CAAGTACTCCCTGATTAAGGGAAATTCATGCCGTCACAGGATGACC 100
|:::||||| |:::||||| |:::||||| |:::||||| |:::|||||
17 sAsnTySerAsnIleGlnGlyAsnHisAlaLeuTyLysAsnAsp 34

101 TGAAGAAATTCCTAGACCGAGCTGCTCAGATATACAGAAAGCGT 150
:::|||||::: |:::|||||::: |:::|||||::: |:::|||||:::
101 TGAAGAAATTCCTAGACCGAGCTGCTCAGATATACAGAAAGCGT 150
::: |:::|||||::: |:::|||||::: |:::|||||::: |:::|||||
51 IleGluAsnLeuPheArgGluLeuAspIleAsnSerAspAsnAlaIleAs 67

201 CTTCAGAGATTCCTCATTCCTGATGAAGAATGGCGCTGGCAGCCACA 250
|:::|||||::: |:::|||||::: |:::|||||::: |:::|||||:::
67 nPheGluGluPheLeuAlaMetValIleLysValGlyValAlaSerHisL 84

251 AAAAAAGCATGAGAA 267
 || |||||
 84 ysaspserrhlslsglu 89

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:AAW03563

seq_documentation_block:

ID AAW03563 standard; Protein; 92 AA.

AC AAW03563;

DT 01-MAY-1997 (first entry)

DE Calcium binding protein CAAFL.

KW Calcium binding protein; bovine; amniotic fluid; S100 protein family;
 KW intracellular signal transduction; squamous epithelial cell; neutrophil;
 KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
 KW squamous cell carcinoma; skin; oesophagus; CAAFL; lung; blood disease.

OS Bos taurus.

PN EP731166-A2.

PD 11-SEP-1996.

PF 04-DEC-1995; 95EP-0119045.

PR 06-MAR-1995; 95JP-0070468.

PR 06-MAR-1995; 95JP-0045564.

PA (HITO/) HITOMI J.

PA (TOFU) TONEN CORP.

PI Hitomi J, Kimura T, Yamaguchi K, Yamamura T;

DR WPI, 1996-403989/41.

DR N-PSDB; AAT39345.

PT New human or bovine calcium binding protein and related nucleic acid

PT - is a marker for inflammation, neoplasia, skin and blood diseases

XX

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4 TTGACCGAGCTGGAGAAAGCCTTGAACCTATCATCAGAGCTCTACACAA 53
 ::|||::|
 1 Methrlyslengluasprhlslengluylleleasnllephelsgl 17

54 GTACTCCCTGATTAAGGCGAATTTCCATGCCGCTACAGGATGACCTGA 103
 :|||::|
 17 ntyrserValargValglYhlspheasprhlleuasnlYsarYglulsl 34

104 AGAATTCCTAGAGACGAGCTGCTCAGTATATCAGG..... 141
 |||::|
 34 ysglneullelthrlYslgluleuprolYstrhlleuglnsnrhlYslasp 50

142 AAAAAAGGTGCAGACGCTGCTTCAAGAGTTGATATCAACACGATGG 191
 ::|||
 51 glnProthrllleasplYsllephelglnasplleuasplaslYslasp 67

192 TGCAGTTAACTTCAGAGCTTCTCATTCGTGATGAAGAAGCGCGTGG 241
 |||||::|
 67 ylaValserPhelglulphelValleuValserArgValleuYsl 84

242 CAGCCCAAAAAAGCATGAGAA 267
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 84 hrlalahlslleaspllehlslsglu 92

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:AAW03564

seq_documentation_block:

ID AAW03564 standard; Protein; 92 AA.

AC AAW03564;

DT 01-MAY-1997 (first entry)

DE Calcium binding protein CAAFL.

KW Calcium binding protein; human; amniotic fluid; S100 protein family;
 KW intracellular signal transduction; squamous epithelial cell; neutrophil;
 KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
 KW squamous cell carcinoma; skin; oesophagus; CAAFL; lung; blood disease.

OS Homo sapiens.

PN EP731166-A2.

PD 11-SEP-1996.

PF 04-DEC-1995; 95EP-0119045.

PR 06-MAR-1995; 95JP-0070468.

PR 06-MAR-1995; 95JP-0045564.

PA (HITO/) HITOMI J.

PA (TOFU) TONEN CORP.

PI Hitomi J, Kimura T, Yamaguchi K, Yamamura T;

DR WPI, 1996-403989/41.

DR N-PSDB; AAT39346.

PT New human or bovine calcium binding protein and related nucleic acid

PT - is a marker for inflammation, neoplasia, skin and blood diseases

XX

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4 TTGACCGAGCTGGAGAAAGCCTTGAACCTATCATCAGAGCTCTACACAA 53
 ::|||::|
 1 Methrlyslengluasprhlslengluylleleasnllephelsgl 17

54 GTACTCCCTGATTAAGGCGAATTTCCATGCCGCTACAGGATGACCTGA 103
 :|||::|
 17 ntyrserValargValglYhlspheasprhlleuasnlYsarYglulsl 34

104 AGAATTCCTAGAGACGAGCTGCTCAGTATATCAGG..... 141
 |||::|
 34 ysglneullelthrlYslgluleuprolYstrhlleuglnsnrhlYslasp 50

142 AAAAAAGGTGCAGACGCTGCTTCAAGAGTTGATATCAACACGATGG 191
 ::|||
 51 glnProthrllleasplYsllephelglnasplleuasplaslYslasp 67

192 TGCAGTTAACTTCAGAGCTTCTCATTCGTGATGAAGAAGCGCGTGG 241
 |||||::|
 67 ylaValserPhelglulphelValleuValserArgValleuYsl 84

242 CAGCCCAAAAAAGCATGAGAA 267
 ::|||
 84 hrlalahlslleaspllehlslsglu 92

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:AAW03564

seq_documentation_block:

ID AAW03564 standard; Protein; 92 AA.

AC AAW03564;

DT 01-MAY-1997 (first entry)

DE Calcium binding protein CAAFL.

KW Calcium binding protein; human; amniotic fluid; S100 protein family;
 KW intracellular signal transduction; squamous epithelial cell; neutrophil;
 KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
 KW squamous cell carcinoma; skin; oesophagus; CAAFL; lung; blood disease.

OS Homo sapiens.

PN EP731166-A2.

PD 11-SEP-1996.

PF 04-DEC-1995; 95EP-0119045.

PR 06-MAR-1995; 95JP-0070468.

PR 06-MAR-1995; 95JP-0045564.

PA (HITO/) HITOMI J.

PA (TOFU) TONEN CORP.

PI Hitomi J, Kimura T, Yamaguchi K, Yamamura T;

DR WPI, 1996-403989/41.

DR N-PSDB; AAT39346.

PT New human or bovine calcium binding protein and related nucleic acid

PT - is a marker for inflammation, neoplasia, skin and blood diseases

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CC infiltrating cancerous lesions. Detection of CAFL (using antibodies in
CC usual immunossays) can be used to diagnose (or monitor) inflammation,
CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,
CC lung and cervix), and skin and blood diseases.
XX
Sequence 92 AA:

[illegible]

alignment_block:
US-09-806-382A-1 x AAW03564 .

Align seg 1/1 to: AAW03564 from: 1 to: 92

[illegible]

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seq_documentation_block:
ID   AAW24137 standard; Protein; 92 AA
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PR DNA encoding chemotactic cytokine I - used to treat, e.g. tumours,
PT chronic infection, leukaemia, etc.
XX
PS Claim 12; Pages 48-49; 64pp; English.

CC This is human chemotactic cytokine I polypeptide. The encoding
CC polypeptide, along with a vector and a host cell can be used for the
CC recombinant production of the chemotactic cytokine. Cytokine agonists
CC and antagonists can be used for the treatment of a patient requiring a
CC chemotactic cytokine I and for the treatment of a patient requiring the
CC inhibition of a chemotactic cytokine I polypeptide, respectively. The
CC chemotactic cytokine is used to treat tumours, chronic infection,
CC leukaemia and T-cell mediated autoimmune diseases.

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alignment_scores:
  quality: 158.00
  ratio: 2.508
  percent_similarity: 65.625
  percent_identity: 38.542
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alignment_block:
US-09-806-382A-1 x AAW24137 ..
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Align seg 1/1 to: AAW24137 from: 1 to: 92

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4  TTGACGAGGTGGGAGAAACCTTTGACCTTTCATGACAGCTTCACGAA 53
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1  MethIyLysLeuIUGuIstIsLeuGluGlyIleValAsnIlePheHisG1 17
54  GTATCCCTCGATTAAGGGAAATTTCCATGCGCGTCTACAGGATGACCTGA 103
   |||.....|.....|.....|.....|.....|.....|.....|.....|
17  nTyLysValAlaIyGlnIAsnIAspPheThrIleuSerYsgIyLysLeuL 34
104  AGAATGCGTACGAGACCGAGTCTCCGATATACAG.....141
   |||.....|.....|.....|.....|.....|.....|.....|.....|
34  ysgIleuLeuThrIySgluIleAlaIAsnThrIleYAsnIleYAsp 50
142  AAAAAGGCTGCAGACGCTGGTTCACAGAGTTGGATATCAACACTATGG 191
   |||.....|.....|.....|.....|.....|.....|.....|.....|
51  LysIleValIleAspIuIlePheGlnIleYAspIAsnGlnAspG1 67
192  TGCAGTAACTTCGACGAGTCTCCGATCTGGTGTATTAAGATGGCGCTGG 241
   |||.....|.....|.....|.....|.....|.....|.....|.....|
67  uGlnIAspPheGlnIuPheIleSerIleVal.....AlaI 80
242  CAGGCCACAAAAAAGCCCTGACAGAAAGCCACAAAG 219
   |||.....|.....|.....|.....|.....|.....|.....|.....|
80  leaIleuYsgIAlaIAsnIstYrHisIstPheIstHisYsgIu 92

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 05:21:34 ; Search time 66.65 Seconds
(without alignments)
1039.290 Million cell updates/sec

Title: US-09-806-382A-1

Perfect score: 282
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Scoring table:
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Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents.NA:*
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	282	100.0	408	1	US-08-385-241-2
2	282	100.0	418	1	US-07-987-272A-15
3	145.8	51.7	4195	1	US-08-200-016-1
4	142.8	50.6	433	1	US-07-987-272A-13
5	65.6	23.3	429	2	US-08-568-310D-1
6	65.6	23.3	429	4	US-09-270-455-1
7	50.8	18.0	273	3	US-08-794-000-3
8	48.4	17.2	441	4	US-08-568-310D-12
9	48.4	17.2	441	4	US-09-270-455-12
10	40.8	14.5	571	1	US-08-385-241-4
11	40	14.2	303	1	US-08-190-560-1
12	40	14.2	303	1	US-08-469-277-1
13	40	14.2	303	2	US-08-468-942-1
14	40	14.2	303	2	US-08-468-942-1
15	40	14.2	579	1	US-08-190-560-3
16	40	14.2	579	1	US-08-469-277-3
17	40	14.2	579	2	US-08-468-946-3
18	40	14.2	579	2	US-08-468-942-3
19	38.2	13.5	10952	1	US-08-602-036A-1
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22	37.4	13.3	4440	1	US-08-200-016-4
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	33	29.8	10.6	1179	4	US-09-027-007-3	Sequence 3, Appl
	34	29.8	10.6	1188	1	US-08-706-539-2	Sequence 2, Appl
	35	29.8	10.6	1188	4	US-09-027-007-2	Sequence 2, Appl
	36	29.8	10.6	1311	1	US-08-706-539-4	Sequence 4, Appl
	37	29.8	10.6	1311	4	US-09-027-007-4	Sequence 4, Appl
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	40	29.8	10.6	1680	1	US-08-488-382A-1	Sequence 1, Appl
	41	29.8	10.6	1680	1	US-08-385-142-1	Sequence 1, Appl
	42	29.8	10.6	1680	2	US-08-480-912-1	Sequence 1, Appl
	43	29.8	10.6	1680	4	US-09-027-007-1	Sequence 1, Appl
	44	29.8	10.6	1692	1	US-08-485-859-1	Sequence 1, Appl
	45	29.8	10.6	1951	3	US-08-895-707-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-385-241-2
; Sequence 2, Application US/08385241
; Patent No. 5776348
; GENERAL INFORMATION:
; APPLICANT: Selenget Ph.D., Jeremy D.
; APPLICANT: Orme-Johnson Ph.D., William H.
; APPLICANT: Dretler M.D., Stephen P.
; APPLICANT: Asakura M.D., Hirokaka
; TITLE OF INVENTION: SYSTEM AND METHOD FOR INHIBITING
; TITLE OF INVENTION: FORMATION OF CRYSTALLINE STRUCTURES THAT INCLUDE STRUVITE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Choate, Hall & Stewart
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,241
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Herschbach Ph.D., Brenda M.
; REGISTRATION NUMBER: P-39,223
; REFERENCE/DOCKET NUMBER: 492611-000 (MIT6915)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hMRP-8 cDNA
; US-08-385-241-2
Query Match 100.0%; Score 282; DB 1; Length 408;

Best Local Similarity 100.0%; Pred. No. 4.2e-87;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 117 CTGATTAAGGGGAAATTTCCATGCCGCTCTACAGGATGACTGGAAGAAATTCCTAGAGACC 176
QY 121 gagtgtccctcaatatacagaagaaagggtgcagacgctcgtgttcaagaagttgatatc 180
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Db 177 GAGTGTCTCTCAGTATATCAGGAAAAAGGTGCAGACGCTGTGTTCAAGAAGTTGATATC 236
QY 181 aacctatggtgagttacttcccaagagttctcattctgtgtgataaagatggcgctg 240
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QY 241 gcaagcccaaaaaaagccatgaagaagccacaagaagtag 282
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```

RESULT 2

US-07-987-272A-15
; Sequence 15, Application US/07987272A
; Patent No. 5731166

GENERAL INFORMATION:

APPLICANT: Gecezy, C., Simpson, R. J. and Lackmann, M
TITLE OF INVENTION: No. 5731166el Chemotactic Factor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cushman Darby & Cushman
STREET: 1100 New York Avenue, N.W., Ninth Floor, East Tower
CITY: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/987,272A
FILING DATE: 05-MAR-1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK 2127
FILING DATE: 05-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 4463
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brinkman, David W
REGISTRATION NUMBER: 20,817
REFERENCE/DOCKET NUMBER: DMB/1925/200259
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861 3000
TELEFAX: 202-822 0944

TELEEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

NAME/KEY: CDS

FEATURE:
LOCATION: 57..218
FEATURE:

NAME/KEY: CDS
LOCATION: 57..335
US-07-987-272A-15

Query Match

100.0%; Score 282; DB 1; Length 418;

Best Local Similarity 100.0%; Pred. No. 4.3e-87;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 57 ATGTTGACCGAGCTGGAGAAAGCCCTTGAACTCATCATGACAGCTACCAAGTACTCTCC 116
QY 61 ctgataaagggaattccatcgctctacaggatgacctgaagaagttagagacc 120
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Db 117 CTGATTAAGGGGAAATTTCCATGCCGCTCTACAGGATGACTGGAAGAAATTCCTAGAGACC 176
QY 121 gagtgtccctcaatatacagaagaaagggtgcagacgctcgtgttcaagaagttgatatc 180
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Db 177 GAGTGTCTCTCAGTATATCAGGAAAAAGGTGCAGACGCTGTGTTCAAGAAGTTGATATC 236
QY 181 aacctatggtgagttacttcccaagagttctcattctgtgtgataaagatggcgctg 240
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Db 237 AACACTGATGTGTCAGTAACTTCCAGGAGTCTCTCATTTCTGTGATTAAGATGGCGCTG 296
QY 241 gcaagcccaaaaaaagccatgaagaagccacaagaagtag 282
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Db 297 GCAGCCCAAAAAAGCCATGAAGAAAGCCACAAAGATAG 338

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RESULT 3

US-08-200-016-1
; Sequence 1, Application US/08200016
; Patent No. 5614397

GENERAL INFORMATION:

APPLICANT: Weissman, Irving
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR MODULATING
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: US
ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,016
FILING DATE: 22-FEB-1994
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 06037/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 4195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-200-016-1

Query Match 51.7%; Score 145.8; DB 1; Length 4195;
Best Local Similarity 95.5%; Pred. No. 5.6e-40;
Matches 150; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 126 tccatgattatcgaagaaggtgcagacgtctggttcaagaagttgatacaaac 185
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Db 2316 tccatgattatcgaagaaggtgcagacgtctggttcaagaagttgatacaaac 2375
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Qy 186 tgaatgagcagtaactccagagattccatctcgtgataaagatgagcagc 245
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Db 2376 tgaatgagcagtaactccagagattccatctcgtgataaagatgagcagc 2435
||||| |

Qy 246 ccaacaaaaagccatgagaagccacacaaagatag 282
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Db 2436 ccacaaaaaaagccatgagaagccacacaaagatag 2472
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RESULT 4
US-07-987-272A-13
; Sequence 13, Application US/07987272A
; Patent No. 5731166
; GENERAL INFORMATION:
; APPLICANT: Geczy, C., Simpson, R. J. and Lackmann, M
; TITLE OF INVENTION: No. 5731166el Chemotactic Factor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman Darby & Cushman
; STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,272A
; FILING DATE: 05-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 2127
; FILING DATE: 05-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 4463
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brickman, David W
; REGISTRATION NUMBER: 20,817
; REFERENCE/DOCKET NUMBER: DMB/1925/200259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861 3000
; TELEFAX: 202-822 0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..318
; US-07-987-272A-13

Query Match 50.6%; Score 142.8; DB 1; Length 433;
Best Local Similarity 71.1%; Pred. No. 1.8e-39;
Matches 189; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 1 atgttgaccgagctggaagaagccttgaaactatcatcagcgtctaccacaagtactcc 60

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Qy 61 ctgaaagggaattccatccgctctacagggatgacctgagaattgtctagagacc 120
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Qy 121 gagtgtccatgatalatcaggaagaaggtgcagacgtctggttcaagaagttgatalc 180
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Qy 241 gcagcccaaaaaagccatgaga 266
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Db 292 gcattctcacaagacagccacaaagga 317
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RESULT 5
US-08-568-310D-1
; Sequence 1, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564(both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 1:
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 429
; US-08-568-310D-1

Query Match 23.3%; Score 65.6; DB 2; Length 429;

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?      TYPE: nucleic acid
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?      STRANDEDNESS: double
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?      TOPOLOGY: linear
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?      MOLECULE TYPE: cdna
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?      PUBLICATION INFORMATION:
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?      RELEVANT RESIDUES IN SEQ ID NO: 1 : FROM 1 TO 429
US-09-270-455-1

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[illegible]

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QY	175	gataacaactgaigtgtgcagttaccttcaggaagttctcctaicttctggtgataaagatg	234
Db	181	GATGCCCAACCGAGGTGACGAGGTCTCTTAAAGGAGTTGTGTGCTGTGGACAGATGTG	240
QY	235	ggcgtgcagcgcacaaaaaaagccatgaa	266
Db	241	CTGATCACAGCCCATGACAACTCCACAAGGA	272

RESULT 8
US-08-568-310D-12
; Sequence 12, Application US/08568310D
; Patent No. 5976832

```

1  APPLICANT: HITOMI, JIRO
2  APPLICANT: YAMAGUCHI, KEN
3  APPLICANT: YAMAMURA, TOKUJIRO
4  APPLICANT: KIMURA, TATSUJI
5  TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
6  NUMBER OF SEQUENCES: 20
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
9  STREET: 99 PARK AVENUE
10 STREET: 6th FLOOR
11 CITY: NEW YORK CITY
12 STATE: NEW YORK
13 COUNTRY: USA
14 ZIP: 10016
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
17 MEDIUM TYPE: STORAGE
18 COMPUTER: IBM-PC COMPATIBLE
19 OPERATING SYSTEM: PC-DOS 6.2
20 SOFTWARE: WORDPERFECT 6.1
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/568, 310D
23 FILING DATE: DECEMBER 6, 1995
24 CLASSIFICATION: 435
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 7-70468 and 7-45564(both Japan)
27 FILING DATE: 3/6/95 and 3/6/95, respectively
28 ATTORNEY/AGENT INFORMATION:
29 NAME: KLEIN, MILTON
30 REGISTRATION NUMBER: 27101
31 REFERENCE/DOCKET NUMBER: 3316
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (212)953-3350
34 TELEFAX: (212)953-3352
35 INFORMATION FOR SEQ ID NO: 12:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 441
38 TYPE: nucleic acid
39 STRANDEDNESS: double
40 TOPOLOGY: linear
41 MOLECULE TYPE: cDNA
42 PUBLICATION INFORMATION:
43 RELEVANT RESIDUES IN SEQ ID NO: 12:
44 RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 441
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QY	61	ctgtataaagggaatttcocatgccgtctacaaggatgtaactgtaagaattgtcagagacc	120
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QY	121	gagtcctccatcatcagaanaaagggtgcagacgtctcgttcaagaagttggaatc	180
Db	139	gagcttggcaaacaccatctcmaaaatattcaaaagttaaacctgtcatgtatgaaatattccaa	198
QY	181	aacactgatgtgcagthaacttcgaagatctcctcatctctgtygataaagaatgggcgtg	240
Db	199	ggccttgatcgttatccaagatgaacagctgacattttcaamaattcatatctccgtgagcc	258
QY	241	gcagcccaaaaaaaagcactgaagaagaagccaaaaagatg	282
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RESULT 9
US-09-270-455-12
; Sequence 12, Application US/09270455
; Patent No. 6313267

APPLICANT: HITOMI, JIRO
 APPLICANT: YAMAGUCHI, KEN
 APPLICANT: YAMAMURA, TOKUJIRO
 APPLICANT: KIMURA, TATSUJI
 TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
 STREET: 99 PARK AVENUE
 STREET: 6th FLOOR
 CITY: NEW YORK CITY
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
 MEDIUM TYPE: STORAGE
 COMPUTER: IBM-PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS 6.2
 SOFTWARE: WORDPERECT 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/270,455
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/568,310
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: KLEIN, MILTON
 REGISTRATION NUMBER: 27101
 REFERENCE/DOCKET NUMBER: 3316
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)953-3350
 TELEFAX: (212)953-3352
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 441
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 POLYMERIZATION INFORMATION:
 RELEVANT RESIDUES IN SEQ ID NO: 12: FROM 1 TO 441

Query Match	17.28;	Score 48.4;	DB 4;	Length 441;
Best Local Similarity	48.28;	Pred. No. 3.5e-07;		
Matches 136; Conservative	0;	Mismatches 146;	Indels 0;	Gaps 0;

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||| | ||||||| ||| | | |||||||
Db 1 ATGGCGTCCCTCTGAGAAAGGCCCTTGATGTGATGTGCACCTTCACAAGTAAGTCTG 60

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 05:22:44 ; Search time 298.43 Seconds

(without alignments)
1622.390 Million cell updates/sec

Title: US-09-806-382A-1

Perfect score: 282

Sequence: 1 atgttgaccgagctgtgagaa.....aagaagaagcaagaagtag 282

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872

Total number of hits satisfying chosen parameters:

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Maximum Match 100%

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18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001C.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	282	100.0	282	21	AAC81808	Human S100A8 CDNA.
2	282	100.0	282	21	AAA11969	Human calcium-bind
3	282	100.0	408	19	AAV34697	Human calprotectin
4	282	100.0	944	22	AAK51509	Human polynucleoti
5	282	100.0	1144	22	AAH73234	Human cervical can
6	282	100.0	1144	22	AAH73234	Human cervical can
7	278.4	98.7	2329	22	AAH72611	Human cervical can
8	249.6	88.5	645	22	AAK52493	Human polynucleoti
9	230.4	81.7	573	22	AAH68950	Human cervical can

10	218.4	77.4	497	22	AAH70917	Human cervical can
11	218.4	77.4	598	22	AAH71815	Human cervical can
12	218.4	77.4	625	22	AAH70613	Human cervical can
13	199	70.6	381	22	AAH71977	Human cervical can
14	199	70.6	512	22	AAH69112	Human cervical can
15	191	67.7	287	22	AAH71248	Human cervical can
16	190	67.4	333	22	AAH69823	Human cervical can
17	145.8	51.7	4195	18	AAH68321	Human multidiug re
18	145.8	51.7	4195	22	AAH68321	Human multidiug re
19	144.8	51.3	254	16	AAH70087	Nucleotide sequenc
20	142.8	50.6	433	13	AAQ23343	Human gene signatu
21	65.6	23.3	429	17	AAH39345	Murine CP-10. Mus
22	61.4	21.8	395	21	AAH62569	Calcium binding pr
23	57	20.2	305	22	AAH71963	Bovine EN-RAGE cDN
24	57	20.2	307	22	AAH69098	Human cervical can
25	57	20.2	358	22	AAH70761	Human cervical can
26	55.8	19.8	273	18	AAH62569	Human S100A5 CDNA.
27	50.8	18.0	273	18	AAH62569	DNA encoding compo
28	50.6	17.9	93	22	AAH71206	Human cervical can
29	50.6	17.9	141	22	AAH72274	Human cervical can
30	50.2	17.8	342	22	AAH54709	Nucleotide sequenc
31	48.4	17.2	440	17	AAH39346	Calcium binding pr
32	48.4	17.2	479	18	AAH85774	Human chemotactic
33	47.6	16.9	279	21	AAH81812	Human S100A12 CDNA
34	46.2	16.4	234	19	AAH47616	Nucleotide sequenc
35	43.2	15.3	573	22	AAH62023	Human foetal liver
36	43.2	15.3	573	22	AAH62023	Probe #7960 for ge
37	43.2	15.3	573	22	AAH10340	Human brain expres
38	43.2	15.3	573	22	AAH36240	Human bone marrow
39	43.2	15.3	573	22	AAH41960	Probe #10646 used
40	43	15.2	524	22	AAH33227	Human colon cancer
41	42.4	15.0	407	23	AAH57328	cDNA #4 encoding p
42	42.2	15.0	712	22	AAH99198	Human protein enco
43	41.8	14.8	273	21	AAH81806	Human S100A6 CDNA.
44	41.8	14.8	452	22	AAH54717	Nucleotide sequenc
45	41.8	14.8	704	20	AAH24438	Human bladder tumo

ALIGNMENTS

RESULT 1	
AC AC81808	standard; cDNA; 282 BP.
XX	
AC AC81808;	
XX	
DT 22-FEB-2001	(first entry)
XX	
DE Human S100A8 CDNA.	
XX	
KW S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;	
KW calcium-binding protein; calcium homeostasis; cardiac muscle;	
KW pumping capacity; myocardial cell; systolic calcium ion release;	
KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;	
KW valve defect; ss.	
XX	
OS Homo sapiens.	
XX	
PN DE19915485-A1.	
XX	
PD 19-OCT-2000.	
XX	
PF 07-APR-1999;	99DE-1015485.
XX	
PR 07-APR-1999;	99DE-1015485.
XX	
PA (KATU/) KATU5 H A.	
XX	
PA (REMP/) REMPPIS A.	
XX	
PI Katus HA, Remppis A;	
XX	
DR WPI; 2000-673510/66.	

DR P-PSDB; AAB45538.
 XX Composition containing S100 protein, corresponding nucleic acid or
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency -
 XX
 XX Claim 36; Page 15; 36pp; German.
 XX
 CC This invention describes a novel composition for treating primary or
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
 CC fragments, or a gene transfer vector containing (II), optionally
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
 CC proteins involved in calcium homeostasis, so their overexpression in
 CC cardiac muscle will improve pumping capacity (and overall capacity) of
 CC the heart. In cultured myocardial cells they increase the contraction and
 CC relaxation rates associated with increased systolic calcium ion release
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
 CC used to treat cardiomyopathy (CMP) where inherited or caused by
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
 CC diastolic CMP caused by toxic/infectious disease, cardiac disease caused
 CC by pulmonary and/or arterial hypertension, and structural disease caused
 CC by rhythm disorders or valve defects, generally any condition associated
 CC with reduced contractile force. Unlike calmodulin, which is expressed
 CC ubiquitously, (I) show tissue-specific expression and treat the
 CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
 CC disease.
 CC
 XX Sequence 282 BP; 90 A; 59 C; 72 G; 61 T; 0 other;
 SQ

Query Match 100.0%; Score 282; DB 21; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1e-80;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaccgagctgagagaagccttgaactctatcatcgagcgtctaccagaactacc 60
 |||||||
 Db 1 atgttaccgagctgagagaagccttgaactctatcatcgagcgtctaccagaactacc 60
 QY 61 ctgataaagggaattcttcacgcgtctacagagatgaccctgaagaatttcctagacc 120
 |||||||
 Db 61 ctgataaagggaattcttcacgcgtctacagagatgaccctgaagaatttcctagacc 120
 QY 121 gagtgcctcagatataatcagaagaagggtgcagacgtctggttcaagaattgatatc 180
 |||||||
 Db 121 gagtgcctcagatataatcagaagaagggtgcagacgtctggttcaagaattgatatc 180
 QY 181 aacactgtgtgctgaacttccagaggttctcattctcgtgtgataaagatggcgctg 240
 |||||||
 Db 181 aacactgtgtgctgaacttccagaggttctcattctcgtgtgataaagatggcgctg 240
 QY 241 gcagcccaaaaaaagcctgaagaagccacaagaagtag 282
 |||||||
 Db 241 gcagcccaaaaaaagcctgaagaagccacaagaagtag 282

RESULT 2

AA11969
 ID AA11969 standard; DNA; 282 BP.

XX AAA11969;

XX 04-AUG-2000 (first entry)

DE Human calcium-binding protein encoding DNA #1.

XX
 KW Calcium-binding protein; granule release; calgranulin; human;
 KW vascular membrane growth; adult respiratory distress syndrome;
 KW acute myocardial infarction; ischemic reperfusion disorder;
 KW glomerulonephritis; rheumatoid arthritis; chronic bronchitis;
 KW cerebral vascular disorder; asthma; peripheral circulation disturbance;
 KW angina pectoris; hypertension; multiple sclerosis; ds.
 XX
 XX Homo sapiens.
 OS

XX
 PN WO200018970-A1.
 XX
 PD 06-APR-2000.
 XX
 XX 28-SEP-1999; 99WO-JP05302.
 XX
 PR 29-SEP-1998; 98JP-0274574.
 XX
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Seto M, Fukuda K;
 XX
 DR WPI: 2000-293189/25.
 DR P-PSDB; AAB7636.
 XX
 PT Controlling the release of granules from cell system using activated
 PT calgranulin for screening substances for granule activating or
 PT inhibiting activity -
 XX
 PS Claim 3(1); Page 37-38; 42pp; Japanese.

CC This invention describes a novel method for controlling the release of
 CC granules by treating a cell system to increase or decrease activated
 CC calgranulin to enhance or depress the release of granules. Calgranulin
 CC is a calcium binding protein and can be used for controlling the release
 CC of granules from a cell system e.g. those involved with the inhibition of
 CC vascular membrane growth. Vascular membrane growth is associated with
 CC e.g. adult respiratory distress syndrome, acute myocardial infarction due
 CC to ischemic reperfusion disorders, glomerulonephritis, rheumatoid
 CC arthritis, chronic bronchitis, cerebral vascular disorders, asthma,
 CC peripheral circulation disturbance, angina pectoris, hypertension and
 CC multiple sclerosis. The new method is used for screening substances for
 CC their ability to activate or inhibit the release of granules. This
 CC sequence encodes a human calcium-binding protein which is described in
 CC the method of the invention.
 CC
 XX Sequence 282 BP; 90 A; 59 C; 72 G; 61 T; 0 other;
 SQ

Query Match 100.0%; Score 282; DB 21; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1e-80;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaccgagctgagagaagccttgaactctatcatcgagcgtctaccagaactacc 60
 |||||||
 Db 1 atgttaccgagctgagagaagccttgaactctatcatcgagcgtctaccagaactacc 60
 QY 61 ctgataaagggaattcttcacgcgtctacagagatgaccctgaagaatttcctagagacc 120
 |||||||
 Db 61 ctgataaagggaattcttcacgcgtctacagagatgaccctgaagaatttcctagagacc 120
 QY 121 gagtgcctcagatataatcagaagaagggtgcagacgtctggttcaagaattgatatc 180
 |||||||
 Db 121 gagtgcctcagatataatcagaagaagggtgcagacgtctggttcaagaattgatatc 180
 QY 181 aacactgtgtgctgaacttccagaggttctcattctcgtgtgataaagatggcgctg 240
 |||||||
 Db 181 aacactgtgtgctgaacttccagaggttctcattctcgtgtgataaagatggcgctg 240
 QY 241 gcagcccaaaaaaagcctgaagaagccacaagaagtag 282
 |||||||
 Db 241 gcagcccaaaaaaagcctgaagaagccacaagaagtag 282

RESULT 3

AAV34697
 ID AAV34697 standard; cDNA; 408 BP.

XX AAV34697;

XX 03-SEP-1998 (first entry)

XX

```

DE Human calprotectin subunit MRP-8 protein encoding cDNA.
XX
XX Human; MRP-8; MRP-14; calprotectin; mineral precipitate; struvite;
KM calcium phosphate; kidney stone; renal calculi; struvite stone;
XX urinary tract infection; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 57..338
FT /*tag= A
FT /product= "human MRP-8"
XX
XX US5776348-A.
XX
XX 07-JUL-1998.
XX
XX 07-FEB-1995; 95US-0385241.
XX
XX 07-FEB-1995; 95US-0385241.
XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Asakura H, Dretler SP, Orme-Johnson WH, Selenkut JD;
XX
XX WPI: 1998-397914/34.
XX
XX P-PSDB: AAM60177.
XX
XX Inhibiting kidney stone formation - uses the protein calprotectin
XX
XX Example 1; Columns 21-22; 19pp; English.
XX
XX This cDNA encodes a human calprotectin subunit MRP-8. This is used in
XX a method for inhibiting the formation of a mineral precipitate in a
XX solution which comprises providing a solution comprising component ions
XX of the mineral precipitate or its precursors and contacting the solution
XX with an effective amount of isolated calprotectin, or a derivative of it.
XX The method is useful for the inhibition of kidney stone formation (renal
XX calculi). Kidney stones are concentrations of inorganic and organic salts
XX that develop though crystal nucleation, aggregation and growth in the
XX kidneys, which then can block the urether and if not passed to the
XX bladder, grow and become symptomatic. Struvite stones (MgNH4PO4) are
XX commonly found after urinary tract infection. The mechanisms of this and
XX other stone formation is unclear, but some urine compositions are known
XX to inhibit formation. One of the major components of these is a protein
XX factor calprotectin, which inhibits mineral precipitation. Calprotectin
XX can also be used to raise antibodies, which in turn can be used to detect
XX the protein in samples. The levels of calprotectin found in samples can
XX be compared to levels found in normal humans, and thus assuming increased
XX calprotectin correlates to indication of kidney stone formation, this
XX procedure can be used as a diagnostic tool.
XX
XX Sequence 408 BP; 118 A; 91 C; 106 G; 93 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 282; DB 19; Length 408;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-80;
XX Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 attttaccgagctggaagaagccttgactatcatcagactctaccacaagatctcc 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 57 atgttgacgagctggaagaagccttgactatcatcagactctaccacaagatctcc 116
XX
XX 61 ctgataaagggaatttcacatgcctctacaaggatgacctggaagaattgtcagaacc 120
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 117 ctgataaagggaatttcacatgcctctacaaggatgacctggaagaattgtcagaacc 176
XX
XX 121 gagtgtctctacgatatcagaagaagggtgcagcagctctggtctcaagaagttgatac 180
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 177 gagtgtctctacgatatcagaagaagggtgcagcagctctggtctcaagaagttgatac 236
XX
XX 181 aacacatggtgcagtttaactccaaggatctcctcatctggtgataaagatgggcgtg 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||

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DB 237 aacacatggtgctgaactccagagcttccatctctggtgataaagatgggcgtg 296
OY 241 gcagcccaaaaaagccatgaagaagccacaagaagtag 282
DB 297 gcagcccaaaaaagccatgaagaagccacaagaagtag 338
XX
XX
XX RESULT 4
XX AAK51509
XX ID AAK51509 standard; cDNA; 944 BP.
XX
XX AAK51509;
XX
XX 06-NOV-2001 (first entry)
XX
XX DE Human polynucleotide SEQ ID NO 54.
XX
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorder; arthritis; inflammation; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200157190-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 05-FEB-2001; 2001WO-US04098.
XX
XX PR 03-FEB-2000; 2000US-0496914.
XX PR 27-APR-2000; 2000US-0560875.
XX PR 20-JUN-2000; 2000US-0598075.
XX PR 19-JUL-2000; 2000US-0620325.
XX PR 01-SEP-2000; 2000US-0654936.
XX PR 15-SEP-2000; 2000US-0663561.
XX PR 20-OCT-2000; 2000US-0693325.
XX PR 30-NOV-2000; 2000US-0728422.
XX
XX PA (HYSEQ-) HYSEQ INC.
XX
XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX PI Xue A, Yang Y, Weinman T, Goodrich R;
XX
XX DR WPI: 2001-476283/51.
XX
XX DR P-PSDB: AAM78376.
XX
XX PT Nucleic acids encoding polypeptides with cytokine-like activities,
XX PT useful in diagnosis and gene therapy -
XX
XX Claim 1; Page 637-638; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine/ cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibitin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 944 BP; 244 A; 231 C; 223 G; 246 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 282; DB 22; Length 944;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-80;

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Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 359 atgttaccgagctggagaaagccttgaacctatcatcagcgtctccacaagtactcc 418
QY 61 ctgataaagggaatttcacatgcgtctacagagatgacccgaagaattgctgaagacc 120
Db 419 ctgataaagggaatttcacatgcgtctacagagatgacccgaagaattgctgaagacc 478
QY 121 gaggtccctcagatatacagaagaaagggtgcagacgtctggtccaaagattgatatc 180
Db 479 gaggtccctcagatatacagaagaaagggtgcagacgtctggtccaaagattgatatc 538
QY 181 aacactgattgtcagattaaactccagaggtctcattctggtgataaagattgagctg 240
Db 539 aacactgattgtcagattaaactccagaggtctcattctggtgataaagattgagctg 598
QY 241 gcaagcccaaaaaaagccatgaagaagacacaaagaagtag 282
Db 599 gcaagcccaaaaaaagccatgaagaagacacaaagaagtag 640
```

RESULT 5

AAH73234

ID AAH73234 standard; cDNA; 1144 BP.

AC AAH73234;

DT 19-SEP-2001 (first entry)

DE Human cervical cancer marker nucleic acid 4508.

KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

OS Homo sapiens.

PN WO200142467-A2.

PD 14-JUN-2001.

PF 08-DEC-2000; 2000WO-US33312.

PR 08-DEC-1999; 99US-0169681.

PR 21-DEC-1999; 99US-0171350.

PR 14-MAR-2000; 2000US-0189315.

PR 12-MAY-2000; 2000US-0203791.

PR 09-JUN-2000; 2000US-0210600.

PR 21-JUL-2000; 2000US-0220114.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Deeds J, Berger A, Zhao X;

DR WPI: 2001-375006/39.

PT New isolated nucleic acid for diagnosing and treating cervical cancer
and for assessing and detecting compounds for treating the cancer -

PS Claim 1; Page 986; 1051pp; English.

XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with
XX cervical cancer or has a pre-malignant condition; to monitor the
XX progression of cervical cancer or a premalignant condition in a patient;
XX and to select and/or assess the efficacy of a compound or therapy for
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy.

SQ Sequence 1144 BP; 347 A; 257 C; 245 G; 295 T; 0 other;

Query Match 100.0%; Score 282; DB 22; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.9e-80;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 atgttaccgagctggagaaagccttgaacctatcatcagcgtctccacaagtactcc 60
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QY 61 ctgataaagggaatttcacatgcgtctacagagatgacccgaagaattgctgaagacc 120
Db 575 ctgataaagggaatttcacatgcgtctacagagatgacccgaagaattgctgaagacc 634
QY 121 gaggtccctcagatatacagaagaaagggtgcagacgtctggtccaaagattgatatc 180
Db 635 gaggtccctcagatatacagaagaaagggtgcagacgtctggtccaaagattgatatc 694
QY 181 aacactgattgtcagattaaactccagaggtctcattctggtgataaagattgagctg 240
Db 695 aacactgattgtcagattaaactccagaggtctcattctggtgataaagattgagctg 754
QY 241 gcaagcccaaaaaaagccatgaagaagacacaaagaagtag 282
Db 755 gcaagcccaaaaaaagccatgaagaagacacaaagaagtag 796
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RESULT 6

AAH73234/C

ID AAH73234 standard; cDNA; 1144 BP.

AC AAH73234;

DT 19-SEP-2001 (first entry)

DE Human cervical cancer marker nucleic acid 4508.

KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

OS Homo sapiens.

PN WO200142467-A2.

PD 14-JUN-2001.

PF 08-DEC-2000; 2000WO-US33312.

PR 08-DEC-1999; 99US-0169681.

PR 21-DEC-1999; 99US-0171350.

PR 14-MAR-2000; 2000US-0189315.

PR 12-MAY-2000; 2000US-0203791.

PR 09-JUN-2000; 2000US-0210600.

PR 21-JUL-2000; 2000US-0220114.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Deeds J, Berger A, Zhao X;

DR WPI: 2001-375006/39.

PT New isolated nucleic acid for diagnosing and treating cervical cancer
and for assessing and detecting compounds for treating the cancer -

PS Claim 1; Page 986; 1051pp; English.

XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with
XX cervical cancer or has a pre-malignant condition; to monitor the
XX progression of cervical cancer or a premalignant condition in a patient;
XX and to select and/or assess the efficacy of a compound or therapy for
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy.

SQ Sequence 1144 BP; 347 A; 257 C; 245 G; 295 T; 0 other;


```
Query Match          100.0%; Score 282; DB 22; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.9e-80;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttgacgaagcttgagaaagccttgaactctatcatcgacgctaccacaagtactcc 60
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DB 436 ATGTTGACCGAGCTGAGAAAGCCCTTGAACTATCATCGACGCTCAACAAGTACTCC 377
    |||||||
QY 61 ctgataaagggaattcccatcgctctacagagatgaacctgaaagaatttgctgaacc 120
    |||||||
DB 376 CTGATTAAGGGCAATTTTCATCCGCTCTACAGGATGACCTGAAGAAATTGCTAGAGACC 317
    |||||||
QY 121 gagtgcctcagatataatcagaagaaagggtgcagacgcttggttcaagaagttgatatc 180
    |||||||
DB 316 GAGTGCTCCTCAGTATATCATGAGAAAGGGTCAAGACGCTGTTCAAGAAGTTGATATC 257
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QY 181 aacctgagtgtgcaagtaacttccaggaagttcctcattctgtgtgataaagatggcggtg 240
    |||||||
DB 256 AACACTGATGTTGAGATTAACTTCACAGAGTTCTCATTTCTGATGAATAAGATGGCGGTG 197
    |||||||
QY 241 gcaagcccaaaaaaagccatgaaagaagccacaagaagtag 282
    |||||||
DB 196 GCAGGCCACAAAAAGCCATGAAGAAAGCCACAAAGATAG 155

RESULT 7
AAH72611
ID AAH72611 standard; cDNA; 2329 BP.
AC AAH72611;
XX
XX 19-SEP-2001 (first entry)
DT
DE Human cervical cancer marker nucleic acid 3885.
DE
XX
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX MO200142467-A2.
XX
XX 14-JUN-2001.
XX
XX
XX 08-DEC-2000; 2000MO-US33312.
XX
XX
XX 08-DEC-1999; 99US-0169681.
XX
XX 21-DEC-1999; 99US-0171350.
XX
XX 14-MAR-2000; 2000US-0189315.
XX
XX 12-MAY-2000; 2000US-0203791.
XX
XX 09-JUN-2000; 2000US-0210600.
XX
XX 21-JUL-2000; 2000US-0220114.
XX
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Deeds J, Berger A, Zhao X;
XX
XX WPI; 2001-37506/39.
XX
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer
XX
XX and for assessing and detecting compounds for treating the cancer -
XX
XX
XX Claim 1; Page 759-760; 1051pp; English.
XX
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX
XX polypeptides are useful: to assess if a patient is afflicted with
XX
XX cervical cancer or has a pre-malignant condition; to monitor the
XX
XX progression of cervical cancer or a premalignant condition in a patient;
XX
XX and to select and/or assess the efficacy of a compound or therapy for
XX
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX
XX useful for gene therapy.
```

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XX
SQ Sequence 2329 BP; 715 A; 398 C; 509 G; 707 T; 0 other;

Query Match          98.7%; Score 278.4; DB 22; Length 2329;
Best Local Similarity 99.6%; Pred. No. 3.6e-79;
Matches 279; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gttgacgaagcttgagaaagccttgaactctatcatcgacgctaccacaagtactcc 62
    |||||||
DB 51 gttgacgaagcttgagaaagccttgaactctatcatcgacgctaccacaagtactcc 110
    |||||||
QY 63 gataaagggaattcccatcgctctacagagatgaacctgaaagaattgctagagaccga 122
    |||||||
DB 111 gataaagggaattcccatcgctctacagagatgaacctgaaagaattgctagagaccga 170
    |||||||
QY 123 gttgcctcagatataatcagaagaaagggtgcagacgcttggttcaagaagttgatatca 182
    |||||||
DB 171 gttgcctcagatataatcagaagaaagggtgcagacgcttggttcaagaagttgatatca 230
    |||||||
QY 183 cactgagtgtgcagtaacttccaggaagttcctcattctgtgtgataaagatggcggtgc 242
    |||||||
DB 231 cactgagtgtgcagtaacttccctggaagttcctcattctgtgtgataaagatggcggtgc 290
    |||||||
QY 243 agcccaaaaaaagccatgaaagaagccacaagaagtag 282
    |||||||
DB 291 agcccaaaaaaagccatgaaagaagccacaagaagtag 330

RESULT 8
AAK52493
ID AAK52493 standard; cDNA; 645 BP.
AC AAK52493;
XX
XX
XX 06-NOV-2001 (first entry)
DT
DE Human polynucleotide SEQ ID NO 2022.
DE
XX
XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
XX
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX
XX Homo sapiens.
XX
XX
XX MO200157190-A2.
XX
XX
XX 09-AUG-2001.
XX
XX
XX 05-FEB-2001; 2001MO-US04098.
XX
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560875.
XX
XX 20-JUN-2000; 2000US-0596075.
XX
XX 19-JUL-2000; 2000US-0620325.
XX
XX 01-SEP-2000; 2000US-0654936.
XX
XX 15-SEP-2000; 2000US-0663561.
XX
XX 20-OCT-2000; 2000US-0693325.
XX
XX 30-NOV-2000; 2000US-0728422.
XX
XX
XX (HYSE-) HYSEQ INC.
XX
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX P-PSDB; AAM79360.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX
XX useful in diagnosis and gene therapy -
XX
XX
```

Pf schlegel K, Deeds J, Berger A, Zhao A,

```
XX DR WPI; 2001-375006/39.
XX PT New isolated nucleic acid for diagnosing and treating cervical cancer
XX PR and for assessing and detecting compounds for treating the cancer -
XX PS Claim 1; Page 463; 1051pp; English.
XX CC The invention relates to novel genes (AAH68727-AAH73383) associated with
XX CC cervical cancer with cytostatic activity. The nucleic acids and encoded
XX CC polypeptides are useful: to assess if a patient is afflicted with
XX CC cervical cancer or has a pre-malignant condition; to monitor the
XX CC progression of cervical cancer or a premalignant condition in a patient;
XX CC and to select and/or assess the efficacy of a compound or therapy for
XX CC inhibiting cervical cancer in a patient. The nucleic acids may also be
XX CC useful for gene therapy.
XX SQ Sequence 497 BP; 150 A; 98 C; 118 G; 131 T; 0 other;

Query Match          77.4%; Score 218.4; DB 22; Length 497;
Best Local Similarity 99.1%; Pred. No. 3.6e-60;
Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 51 caagtactccctgataaagggaatttcacatgcgctctacagagatgacctgaagaatt 110
   11 |||||||
DB 36 caggtactccctgataaagggaatttcacatgcgctctacagagatgacctgaagaatt 95
   |||||||
OY 111 gctagaagaccgagtgctccctcagtatatcaggaagaagggtgcagacgtctgttcaaga 170
   |||||||
DB 96 gctagaagaccgagtgctccctcagtatatcaggaagaagggtgcagacgtctgttcaaga 155
   |||||||
OY 171 gttgatatcaaacactgagtgtgcagtttaacttcagagagttccctcattctgtgataaa 230
   |||||||
DB 156 gttgatatcaaacactgagtgtgcagtttaacttcagagagttccctcattctgtgataaa 214
   |||||||
OY 231 gatggcgctgagcagcccaaaaagccatgaagaagcccaagaagtgat 282
   |||||||
DB 215 gatggcgctgagcagcccaaaaagccatgaagaagcccaagaagtgat 266

RESULT 11
AAH71815
ID AAH71815 standard; cDNA; 598 BP.
XX AC AAH71815;
XX DT 19-SEP-2001 (first entry)
XX DE Human cervical cancer marker nucleic acid 3089.
XX KM Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX OS Homo sapiens.
XX PN WO200142467-A2.
XX PD 14-JUN-2001.
XX PF 08-DEC-2000; 2000MO-US33312.
XX PR 08-DEC-1999; 99US-0169681.
XX PR 21-DEC-1999; 99US-0171350.
XX PR 14-MAR-2000; 2000US-0189315.
XX PR 12-MAY-2000; 2000US-0203791.
XX PR 09-JUN-2000; 2000US-0210600.
XX PR 21-JUL-2000; 2000US-0220114.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PT Schlegel R, Deeds J, Berger A, Zhao X;
XX DR WPI; 2001-375006/39.
```

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XX DR New isolated nucleic acid for diagnosing and treating cervical cancer
XX PT and for assessing and detecting compounds for treating the cancer -
XX PS Claim 1; Page 616; 1051pp; English.
XX CC The invention relates to novel genes (AAH68727-AAH73383) associated with
XX CC cervical cancer with cytostatic activity. The nucleic acids and encoded
XX CC polypeptides are useful: to assess if a patient is afflicted with
XX CC cervical cancer or has a pre-malignant condition; to monitor the
XX CC progression of cervical cancer or a premalignant condition in a patient;
XX CC and to select and/or assess the efficacy of a compound or therapy for
XX CC inhibiting cervical cancer in a patient. The nucleic acids may also be
XX CC useful for gene therapy.
XX SQ Sequence 598 BP; 179 A; 113 C; 158 G; 148 T; 0 other;

Query Match          77.4%; Score 218.4; DB 22; Length 598;
Best Local Similarity 99.1%; Pred. No. 3.9e-60;
Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 51 caagtactccctgataaagggaatttcacatgcgctctacagagatgacctgaagaatt 110
   11 |||||||
DB 12 caggtactccctg-taaagggaatttcacatgcgctctacagagatgacctgaagaatt 70
   |||||||
OY 111 gctagaagaccgagtgctccctcagtatatcaggaagaagggtgcagacgtctgttcaaga 170
   |||||||
DB 71 gctagaagaccgagtgctccctcagtatatcaggaagaagggtgcagacgtctgttcaaga 130
   |||||||
OY 171 gttgatatcaaacactgagtgtgcagtttaacttcagagagttccctcattctgtgataaa 230
   |||||||
DB 131 gttgatatcaaacactgagtgtgcagtttaacttcagagagttccctcattctgtgataaa 190
   |||||||
OY 231 gatggcgctgagcagcccaaaaagccatgaagaagcccaagaagtgat 282
   |||||||
DB 191 gatggcgctgagcagcccaaaaagccatgaagaagcccaagaagtgat 242

RESULT 12
AAH70613
ID AAH70613 standard; cDNA; 625 BP.
XX AC AAH70613;
XX DT 19-SEP-2001 (first entry)
XX DE Human cervical cancer marker nucleic acid 1887.
XX KM Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX OS Homo sapiens.
XX PN WO200142467-A2.
XX PD 14-JUN-2001.
XX PF 08-DEC-2000; 2000MO-US33312.
XX PR 08-DEC-1999; 99US-0169681.
XX PR 21-DEC-1999; 99US-0171350.
XX PR 14-MAR-2000; 2000US-0189315.
XX PR 12-MAY-2000; 2000US-0203791.
XX PR 09-JUN-2000; 2000US-0210600.
XX PR 21-JUL-2000; 2000US-0220114.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PT Schlegel R, Deeds J, Berger A, Zhao X;
XX DR WPI; 2001-375006/39.
XX DR New isolated nucleic acid for diagnosing and treating cervical cancer
```

PT and for assessing and detecting compounds for treating the cancer -
PS Claim 1; Page 406-407; 1051pp; English.
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy.
XX
XX Sequence 625 BP; 184 A; 119 C; 167 G; 155 T; 0 other;
SQ
Query Match 77.4%; Score 218.4; DB 22; Length 625;
Best Local Similarity 99.1%; Pred. No. 3.9e-60;
Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 51 caagtactccctgataaagggaatttcacatgcgcgtctacaggaatgacctgaagaatt 110
|||
DB 39 caggtactccctg-taaagggaatttcacatgcgcgtctacaggaatgacctgaagaatt 97
OY 111 gctagagacccgagtgctctcagtatatcaggaataagggtgcagacgtctgttcaaga 170
|||
DB 98 gctagagacccgagtgctctcagtatatcaggaataagggtgcagacgtctgttcaaga 157
OY 171 gctgataatcaacactgtatgtgcagtttaacttccaggaattccctcattctgtgataa 230
|||
DB 158 gctgataatcaacactgtatgtgcagtttaacttccaggaattccctcattctgtgataa 217
OY 231 gatggcgctgagcccaaaaaaagccatgagaagaagccacaagaagagag 282
|||
DB 218 gatggcgctgagcccaaaaaaagccatgagaagaagccacaagaagagag 269
RESULT 13
AAH71977
ID AAH71977 standard; cDNA; 381 BP.
XX
XX AAH71977;
AC
XX 19-SEP-2001 (first entry)
DT
XX Human cervical cancer marker nucleic acid 3251.
DE
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
KW
XX Homo sapiens.
OS
XX WO200142467-A2.
PN
XX 14-JUN-2001.
PD
XX 08-DEC-2000; 2000WO-US33312.
PF
XX 08-DEC-1999; 99US-0169681.
PR 21-DEC-1999; 99US-0171350.
PR 14-MAR-2000; 2000US-0189315.
PR 12-MAY-2000; 2000US-0203791.
PR 09-JUN-2000; 2000US-0210600.
PR 21-JUL-2000; 2000US-0220114.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Deeds J, Berger A, Zhao X;
PI
XX WPI; 2001-375006/39.
DR
XX New isolated nucleic acid for diagnosing and treating cervical cancer
PT and for assessing and detecting compounds for treating the cancer -
XX

PS Claim 1; Page 638; 1051pp; English.
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy.
XX
XX Sequence 381 BP; 116 A; 78 C; 90 G; 97 T; 0 other;
SQ
Query Match 70.6%; Score 199; DB 22; Length 381;
Best Local Similarity 96.6%; Pred. No. 5.5e-54;
Matches 225; Conservative 0; Mismatches 5; Indels 3; Gaps 2;
OY 51 caagtactccctgataaagggaatttcacatgcgcgtctacaggaatgacctgaagaatt 110
|||
DB 10 caggtactccctgataaagggaatttcacatgcgcgtctacaggaatgacctgaagaatt 69
OY 111 gctagagacccgagtgctctcagtatatcaggaataagggtgcagacgtctgttcaaga 170
|||
DB 70 gctagagacccgagtgctctcagtatatcaggaataagggtgcagacgtctgttcaaga 129
OY 171 gctgataatcaacactgtatgtgcagtttaacttccaggaattccctcattctgtgataa 230
|||
DB 130 gctgataatcaacactgtatgtgcagtttaacttccaggaattccctcattctgtgataa 187
OY 231 gatggc-gtggcagcccaaaaaaagccatgagaagaagccacaagaagagag 282
|||
DB 188 gatggcgtggcagcccaaaaaaagccatgagaagaagccacaagaagagag 240
RESULT 14
AAH69112
ID AAH69112 standard; cDNA; 512 BP.
XX
XX AAH69112;
AC
XX 19-SEP-2001 (first entry)
DT
XX Human cervical cancer marker nucleic acid 386.
DE
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
KW
XX Homo sapiens.
OS
XX WO200142467-A2.
PN
XX 14-JUN-2001.
PD
XX 08-DEC-2000; 2000WO-US33312.
PF
XX 08-DEC-1999; 99US-0169681.
PR 21-DEC-1999; 99US-0171350.
PR 14-MAR-2000; 2000US-0189315.
PR 12-MAY-2000; 2000US-0203791.
PR 09-JUN-2000; 2000US-0210600.
PR 21-JUL-2000; 2000US-0220114.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Deeds J, Berger A, Zhao X;
PI
XX WPI; 2001-375006/39.
DR
XX New isolated nucleic acid for diagnosing and treating cervical cancer
PT and for assessing and detecting compounds for treating the cancer -
XX
XX Claim 1; Page 170-171; 1051pp; English.
PS

CC The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy.

SQ Sequence 512 BP; 156 A; 103 C; 117 G; 134 T; 2 other;

Query Match

Best Local Similarity 70.6%; Score 199; DB 22; Length 512;

Matches 225; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 51 caaagtacccctgataaagggaattccatgccttcacaggaatgagccgaagaatt 110
DB 26 caagtaacctccctgataaagggaattccatgccttcacaggaatgagccgaagaatt 85
QY 111 gctagagaccgagtgctcctcagatatacaggaaaaagggtgcagacgtctgtccaaga 170
DB 86 gctagagaccgagtgctcctcagatatacaggaaaaagggtgcagacgtctgtccaaga 145
QY 171 gttgatatcaacacacgagtgatcacttcacaggaaggtccctccttcctgtgataaa 230
DB 146 gttgatatcaacacacgagtgatcacttcacaggaaggtccctccttcctgtgataaa 203
QY 231 gatggg-cgtggcagcccaaaaagccatgaagaagaagccacaaagaatag 282
DB 204 gatgggcgtggcagcccaaaaagccatgaagaagaagccacaaagaatag 256

RESULT 15

ID AAH71248/c
AAH71248 standard; cDNA: 297 BP.

AC AAH71248;

DT 19-SEP-2001 (first entry)

DE Human cervical cancer marker nucleic acid 2522.

KW Cervical cancer: cytostatic; pre-malignant condition; gene therapy; ss.

OS Homo sapiens.

PN MO200142467-A2.

PD 14-JUN-2001.

PF 08-DEC-2000; 2000MO-US33312.

PR 08-DEC-1999; 99US-0169681.

PR 21-DEC-1999; 99US-0171350.

PR 14-MAR-2000; 2000US-0189315.

PR 12-MAY-2000; 2000US-0203791.

PR 09-JUN-2000; 2000US-0210600.

PR 21-JUL-2000; 2000US-0220114.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Deeds J, Berger A, Zhao X;

DR WPI: 2001-375006/39.

PT New isolated nucleic acid for diagnosing and treating cervical cancer
PT and for assessing and detecting compounds for treating the cancer -

PS Claim 1; Page 525; 1051pp; English.

CC The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded

CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy.

SQ Sequence 297 BP; 66 A; 77 C; 66 G; 88 T; 0 other;

Query Match

Best Local Similarity 67.7%; Score 191; DB 22; Length 297;

Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ggaatgacctgagaagaattgctagagaccgagtgctcctcagatatacaggaagaagggtc 151
DB 297 ggaatgacctgagaagaattgctagagaccgagtgctcctcagatatacaggaagaagggtc 238
QY 152 cgaagctcgtgtcaaaagattgatatcaacactgaatggtgaattacttcaggagt 211
DB 237 cgaagctcgtgtcaaaagattgatatcaacactgaatggtgaattacttcaggagt 178
QY 212 tctcatctcgtgtgaataagatgagcgtgagcccaaaaaaagccatgaagaagcc 271
DB 177 tctcatctcgtgtgaataagatgagcgtgagcccaaaaaaagccatgaagaagcc 118
QY 272 acaaaagatag 282
DB 117 ACAAAAGATAG 107

Search completed: September 10, 2002, 06:49:27
Job time: 5203 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 04:17:24 ; Search time 2463.79 Seconds

(without alignments)
1544.832 Million cell updates/sec

Title: US-09-806-382A-1

Perfect score: 282
Sequence: 1 atgttgaccgagctcgagaa.....aagaagccacaagagtag 282

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em.estba:*
2: em.esthum:*
3: em.estin:*
4: em.estmu:*
5: em.estcov:*
6: em.estpl:*
7: em.estro:*
8: em.htc:*
9: gb.estl:*
10: gb.estc2:*
11: gb.htc:*
12: gb.gss:*
13: em.gss.hum:*
14: em.gss.inv:*
15: em.gss.dln:*
16: em.gss.vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	282	100.0	324	9	AA086471 zn62b01.s
C 2	282	100.0	325	9	AA086471 zn62b01.s
C 3	282	100.0	337	9	AA584358 nm73d05.s
C 4	282	100.0	361	10	F24145 HSPD10203.H
C 5	282	100.0	369	9	AA086471 zn62b01.s
C 6	282	100.0	376	9	AA086471 zn62b01.s
C 7	282	100.0	376	9	AA086471 zn62b01.s
C 8	282	100.0	377	9	AA086471 zn62b01.s
C 9	282	100.0	380	9	AA086471 zn62b01.s
C 10	282	100.0	384	9	AA086471 zn62b01.s
C 11	282	100.0	384	10	BF478287 nae46g08.x
C 12	282	100.0	386	9	AA086471 zn62b01.s
C 13	282	100.0	388	9	AA086471 zn62b01.s
C 14	282	100.0	389	9	AA086471 zn62b01.s
C 15	282	100.0	390	10	W79564
C 16	282	100.0	391	9	AA086471 zn62b01.s
C 17	282	100.0	394	9	AA086471 zn62b01.s

18	282	100.0	396	9	AA086471 zn62b01.s
19	282	100.0	396	9	AA086471 zn62b01.s
20	282	100.0	397	9	AA086471 zn62b01.s
21	282	100.0	398	9	AA086471 zn62b01.s
22	282	100.0	399	9	AA086471 zn62b01.s
C 23	282	100.0	400	9	AA086471 zn62b01.s
C 24	282	100.0	400	10	BG684273
C 25	282	100.0	404	9	AA086471 zn62b01.s
C 26	282	100.0	406	9	AA086471 zn62b01.s
C 27	282	100.0	406	9	AA086471 zn62b01.s
C 28	282	100.0	407	9	AA086471 zn62b01.s
C 29	282	100.0	407	10	BG743273
C 30	282	100.0	410	9	AA086471 zn62b01.s
C 31	282	100.0	410	10	BM007720
C 32	282	100.0	414	9	AA086471 zn62b01.s
C 33	282	100.0	416	9	AA086471 zn62b01.s
C 34	282	100.0	416	9	AA086471 zn62b01.s
C 35	282	100.0	418	9	AA086471 zn62b01.s
C 36	282	100.0	419	9	AA086471 zn62b01.s
C 37	282	100.0	419	10	B1909815
C 38	282	100.0	420	9	AA086471 zn62b01.s
C 39	282	100.0	421	9	AA086471 zn62b01.s
C 40	282	100.0	422	9	AA086471 zn62b01.s
C 41	282	100.0	423	9	AA086471 zn62b01.s
C 42	282	100.0	424	9	AA086471 zn62b01.s
C 43	282	100.0	427	9	AA086471 zn62b01.s
C 44	282	100.0	428	9	AA086471 zn62b01.s
C 45	282	100.0	428	9	AA086471 zn62b01.s

ALIGNMENTS

RESULT 1
LOCUS AA086471/c
DEFINITION zn62b01.s1 StrataGene muscle 937209 Homo sapiens cDNA clone
IMAGE:562729 3' similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);
RNA sequence.
AA086471.1 GI:1629088
EST.

ACCESSION AA086471.1 GI:1629088
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoe,S., Dietrich,N., Dubuque,T., Favellio,A., Gish,M., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierly-Meg,D., Trevisan,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R., and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE JOURNAL
MEDLINE
COMMENT
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Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 450 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham.

FEATURES

Location/Qualifiers
1..324
/organism="Homo sapiens"
/db_xref="GDB:4596019"
/db_xref="taxon:9606"
/clone="IMAGE:562729"
/clone_lib="StrataGene muscle 937209"

/tissue_type="muscle"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skeletal muscle; Vector: pBluescript SK-
site.1: EcoRI; site.2: XhoI; Cloned unidirectionally.
Primer: Oligo dt. Skeletal muscle from patient with
malignant hyperthermia. Average insert size: 1.0 kb;
uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAAATCGGCGACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'"

BASE COUNT 70 a 84 c 70 g 97 t 3 others
ORIGIN

Query Match 100.0%; Score 282; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttgaaccgagcttgagaagccttgaactctatcatcagcgtctaccacaagtactcc 60
|||||
DB 321 ATGTTGACCGAGCTGGAGAAAGCCTTGACTCTATCATCGACGCTACCAAGTACTCC 262
QY 61 ctgataaagggaattccatccgctctcaaggagatgacctgaagaattgctagagacc 120
|||||
DB 261 CTGATTAAGGGGAATTTCCATGCGCTCTACAGGATGACCTGAAGAATTGCTAGAGACC 202
QY 121 gagtgcctcagtatatcaggaagagggtgcagagcgtctggttcaagaggttgatattc 180
|||||
DB 201 GAGTGTCTCAGTATATCAGAAAAAGGTGCAAGACTCTGTTCAAGAGTTGATATC 142
QY 181 aacctgatgtgtagttaaacttccaggagttctcattctgtgtataaagatggcgctg 240
DB 141 AACACTGATGTGTGAGTTAACTTCACAGAGTTCTCTCATTCGTGATTAAGATGGCGGTG 82
QY 241 gcagcccaaaaaaagccatgaagaagccacaaagagtag 282
DB 81 GCAGCCCAAAAAAGCCATGAAGAAAGCCACAAAGAGTAG 40

RESULT 2
AM238704 325 bp mRNA linear EST 13-DEC-1999
LOCUS
DEFINITION xp30e12.x1 NCI-CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741902 3'
similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);, mRNA sequence.
AM238704
ACCESSION AM238704.1 GI:6571093
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 325)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Edward Shillito Ph.D., Silvio Gutkind Ph.D.,
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES
SOURCE
Possible reversed clone: polyT not found
Seq primer: -40UP from Gidco
High quality sequence stop: 301.
Location/Qualifiers
1..325
/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone="IMAGE:2741902"
/clone_lib="NCI CGAP_HN10"
/tissue_type="carcinoma in situ from retroocular trigone"
/lab_host="DH10B"
/note="Vector: pAMP10; cDNA made by Oligo-dT priming.
Non-directionally cloned into the UDG sites of pAMP10.
Size-selected on agarose gel, average insert size 500 bp.
Primary library; non-amplified. CDNA Library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 96 a 72 c 89 g 68 t
ORIGIN

Query Match 100.0%; Score 282; DB 9; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttgaaccgagcttgagaagccttgaactctatcatcagcgtctaccacaagtactcc 60
|||||
DB 16 ATGTTGACCGAGCTGGAGAAAGCCTTGAACTCTATCATCGACGCTACCAAGTACTCC 75
QY 61 ctgataaagggaattccatccgctctcaaggagatgacctgaagaattgctagagacc 120
|||||
DB 76 CTGATTAAGGGGAATTTCCATGCGCTCTACAGGATGACCTGAAGAATTGCTAGAGACC 135
QY 121 gagtgcctcagtatatcaggaagagggtgcagagcgtctggttcaagaggttgatattc 180
|||||
DB 136 GAGTGTCTCAGTATATCAGAAAAAGGTGCAAGCTGTGTTCAAGAGTTGATATC 195
QY 181 aacctgatgtgtagttaaacttccaggagttctcattctgtgtataaagatggcgctg 240
DB 196 AACACTGATGTGTGAGTTAACTTCACAGAGTTCTCTCATTCGTGATTAAGATGGCGGTG 255
QY 241 gcagcccaaaaaaagccatgaagaagccacaaagagtag 282
DB 256 GCAGCCCAAAAAAGCCATGAAGAAAGCCACAAAGAGTAG 297

RESULT 3
AA584358/c 337 bp mRNA linear EST 26-SEP-1997
LOCUS
DEFINITION AA584358.n1 NCI-CGAP_Lari Homo sapiens cDNA clone IMAGE:1089515 3'
similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);, mRNA sequence.
AA584358
ACCESSION AA584358.1 GI:2368967
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 337)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES
SOURCE
Possible reversed clone: polyT not found
Seq primer: -40m13 fwd. ET from Amerisham.
Insert Length: 534 Std Error: 0.00
Location/Qualifiers
1..337
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1089515"

/clone.lib="NCI-CGAP_Lar1"
/issue_type="larynx"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: larynx; Vector: Bluescript SK-; Site: 1:
EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer:
0.1µg dt. larynx. 5' adaptor sequence: 5' GATTCGGCAGC
3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTT 3'
Average insert size: 0.9 kb."
BASE COUNT 73 a 89 c 76 g 99 t
ORIGIN

Query Match 100.0%; Score 282; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgttaccgagcttgagaagccttgaaactatcatcagcgtctacacaagttactcc 60
DB 323 ATGTTGACCGAGCTGGAGAAAGCCTTGAACTCATCATGAGCTTACCAAGTACTCC 264
QY 61 ctgataaagggaatttcacatgcgcgtctacaggagatgacctaagaattgtctagaagcc 120
DB 263 CTGATTAAGGGGAATTTCCATGCCGCTCTACAGGAGATGACCTGAAGAAATTTGCTAGAGACC 204
QY 121 gaatgtcctcagatatacaggaagaaaggctgacagcgtctggttcaaaagagtttgatalc 180
DB 203 GAGTGTCTCAGTATATACAGGAAAGGGTGACAGACGTCTGTTCAAGAGTTGGATATC 144
QY 181 aacactgatgtgcaattactccagagagttccattctcgtgtgataaagatggcgtg 240
DB 143 AACCTGATGCTCAGTATTAATCTCCAGGAGTTCCTCATTTCTGTATTAAGATGGCGGTG 84
QY 241 gcagcccaaaaaaaagccatgagaagaaagccacaagagtag 282
DB 83 GCAGCCCAAAAAAGCCATGAAGAAAGCCAAAGAGTAG 42

RESULT 4
F24145 361 bp mRNA linear EST 13-MAY-1999
LOCUS HSPD10203 HM3 Homo sapiens cDNA clone s4000003611, mRNA sequence.
DEFINITION F24145
ACCESSION F24145.1 GI:4809771
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 361)
AUTHORS Lanfranchi, G., Muraro, T., Caldera, F., Pachioni, B., Pallavicini, A.,
Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.
TITLE Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization
JOURNAL Genome Res. 6 (1), 35-42 (1996)
MEDLINE 96276048
COMMENT Contact: Valle G.
CIRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
http://grip.bio.unipd.it.
LOCATION/Qualifiers
1. 361
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000003611"
/clone.lib="HM3"
/sex="female"
/issue_type="pectoral muscle (after mastectomy)"
/note="Vector: pCDNAII (Invitrogen); Site: 1: BstXI;
Site: 2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.

The first strand cDNA was primed with a biotinylated
0.1µg-dt-NOTI primer
(5'-biotin-AACCGGCTCGACGGCCGCTTTTCTTTTCTTTT-3'). The
ds cDNA was sonicated and size-selected in the range
350-550 bp. The 3' specific fragments were selected by
streptavidin coated magnetic beads, ligated to
non-palindromic BstXI adaptors, NOTI digested and
directionally cloned into BstXI-NOTI cut pCDNAII vector."
BASE COUNT 106 a 80 c 100 g 75 t
ORIGIN

Query Match 100.0%; Score 282; DB 10; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgttaccgagcttgagaagccttgaaactatcatcagcgtctacacaagttactcc 60
DB 32 ATGTTGACCGAGCTGGAGAAAGCCTTGAACTCATCATGAGCTTACCAAGTACTCC 91
QY 61 ctgataaagggaatttcacatgcgcgtctacaggagatgacctaagaattgtctagaagcc 120
DB 92 CTGATTAAGGGGAATTTCCATGCCGCTCTACAGGAGATGACCTGAAGAAATTTGCTAGAGACC 151
QY 121 gaatgtcctcagatatacaggaagaaaggctgacagcgtctggttcaaaagagtttgatalc 180
DB 152 GAGTGTCTCAGTATATACAGGAAAGGGTGACAGACGTCTGTTCAAGAGTTGGATATC 211
QY 181 aacactgatgtgcaattactccagagagttccattctcgtgtgataaagatggcgtg 240
DB 212 AACCTGATGCTCAGTATTAATCTCCAGGAGTTCCTCATTTCTGTATTAAGATGGCGGTG 271
QY 241 gcagcccaaaaaaaagccatgagaagaaagccacaagagtag 282
DB 272 GCAGCCCAAAAAAGCCATGAAGAAAGCCAAAGAGTAG 313

RESULT 5
AW265292 369 bp mRNA linear EST 28-DEC-1999
LOCUS x949h08.x1 NCI-CGAP_HN7 Homo sapiens cDNA clone IMAGE:2754015 3'
DEFINITION similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);, mRNA sequence.
ACCESSION AW265292
VERSION AW265292.1 GI:6642108
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,
Childanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILM at:
www-bio.llnl.gov/bdrp/image/image.html

FEATURES
source
possible reversed clone: polyT not found
Seq primer: -40up from gibco.
Location/Qualifiers
1. 369
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2754015"
/clone.lib="NCI-CGAP_HN7"

/tissue_type="normal squamous epithelium, floor of mouth"
/lab_host="DH10B"
/note="Vector: PAMP10; cDNA made by oligo-dT priming.
/non-directionally cloned into the UDG sites of PAMP10.
Size-selected on agarose gel, average insert size 500 bp.
Primary library; non-amplified. cDNA library
Preparation: David B. Krizman, Ph.D. (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT 111 a 84 c 96 g 78 t
ORIGIN

Query Match 100.0%; Score 282; DB 9; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaccagctgtgagaagccttgaaactctatcatcgaagcttaccagaagttacc 60
|||||
Db 20 ATGTTGACCGAGCTGGAGAAAGCCTTGAACTCATCATGAGCTGTACACAAAGTACTCC 79
QY 61 ctgataaagggaattccatgcgctctacaggaatgacctgaagaattgctagaagcc 120
|||||
Db 80 CTGATTAAGGGGAATTCCATGCGCTCTACAGGATGACCTGAAGAATTGCTAGAGACC 139
QY 121 gattgtcctcagatatcagaaaagggtgcagagctgtgttcaaaagattgatac 180
|||||
Db 140 GAGGTCTCTAGTATATCAGAAAAGGCTGCAAGCTCTGTTCAAAAGTTGGATATC 199
QY 181 aacactgattgtcagttactccaggaattcctcatcttggtgataaagatggcggtg 240
|||||
Db 200 AACACTGATGGTGAGTACTTCCAGAGAGTCTCATCTGTGATTAAGATGGCGGTG 259
QY 241 gcaagcccaaaaaagccatgaagaagcccaaaagatgag 282
|||||
Db 260 GCAGCCCAACAAAAAGCCATGAAGAGCCACAAAGATGAG 301

RESULT 6
BE139192/c 369 bp mRNA linear EST 21-JUN-2000
LOCUS BE139192
DEFINITION xp38610.x2 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752915 3'
similar to gb:A12027_cdsl CALGRANULIN A (HUMAN);, mRNA sequence.
ACCESSION BE139192
VERSION BE139192.1 GI:8601615
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 369)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

REFERENCE
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgapbs-remail.nih.gov
COMMENT Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.lnl.gov
Seq primer: -40up from Gibco.

FEATURES
source Location/Qualifiers
1. 369

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2752915"
/clone_lib="NCI_CGAP_Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"

/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: SalI;
Site_2: NotI. Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
BASE COUNT 79 a 95 c 83 g 112 t
ORIGIN

Query Match 100.0%; Score 282; DB 9; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaccagctgtgagaagccttgaaactctatcatcgaagcttaccagaagttacc 60
|||||
Db 352 ATGTTGACCGAGCTGGAGAAAGCCTTGAACTCATCATGAGCTGTACACAAAGTACTCC 293
QY 61 ctgataaagggaattccatgcgctctacaggaatgacctgaagaattgctagaagcc 120
|||||
Db 292 CTGATTAAGGGGAATTCCATGCGCTCTACAGGATGACCTGAAGAATTGCTAGAGACC 233
QY 121 gattgtcctcagatatcagaaaagggtgcagagctgtgttcaaaagattgatac 180
|||||
Db 232 GAGTCTCTCACTATATATCAGAAAAGGCTGCAAGCTGTGTTCAAAAGTGTGATATC 173
QY 181 aacactgattgtcagttactccaggaattcctcatcttggtgataaagatggcggtg 240
|||||
Db 172 AACACTGATGGTGAGTACTTCCAGAGAGTCTCATCTGTGATTAAGATGGCGGTG 113
QY 241 gcaagcccaaaaaagccatgaagaagcccaaaagatgag 282
|||||
Db 112 GCAGCCCAACAAAAAGCCATGAAGAGCCACAAAGATGAG 71

RESULT 7
AM238650/c 376 bp mRNA linear EST 13-DEC-1999
LOCUS AM238650
DEFINITION xp29f02.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741787 3'
similar to gb:A12027_cdsl CALGRANULIN A (HUMAN);, mRNA sequence.
ACCESSION AM238650
VERSION AM238650.1 GI:5571039
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 376)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

REFERENCE
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgapbs-remail.nih.gov
COMMENT Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html

FEATURES
source Location/Qualifiers
1. 376

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2741787"
/clone_lib="NCI_CGAP_HN10"
/tissue_type="carcinoma in situ from retromolar trigone"
/lab_host="DH10B"
/note="Vector: PAMP10; cDNA made by oligo-dT priming.
Non-directionally cloned into the UDG sites of PAMP10.

Size-selected on agarose gel, average insert size 500 bp.
Primary library: non-amplified. cDNA library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 77 a 92 c 81 g 126 t

ORIGIN

Query Match 100.0%; Score 282; DB 9; Length 376;
Best Local Similarity 100.0%; Pred. No. 1,8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaccgagcttggagaagccttgaactctatcaltcagcgtctaccacaagtactcc 60
DB 376 ATGTGACCGAGCTGGAGAAAGCCTTGAACTCTATCATCGAGCTACCAACTACTCC 317
QY 61 ctgataaagggaattccatgcgcgtctacaggagatgacctgaagaattgtctagacc 120
DB 316 CTGATTAAGGGGAATTTCCATGCCCTTACAGGATGACGTAAGAAATTCCTAGAGACC 257
QY 121 gagtgcctcagtatatcaggaaaagggtgcagcgtctgttcaagaagtgtatatac 180
DB 256 GAGTGTCTCTCACTATATATAGCAAAAAGGCTGACAGCTGTCTGTTCAAGAATTGGATATC 197
QY 181 aacactgatgtgcagtaacttccaggagttcctcattctgtgtatataaagtggcgtg 240
DB 196 AACACTGATGGTGGAGTTAACTTCCAGAGTTCTCATTTCTGGATTAAGATGGGCGCTG 137
QY 241 gcagcccaaaaaaagccatgagaagaagccacaagaagttag 282
DB 136 GCAGCCACAAAAAAGCCATGAAGAAAGCCACAAAGATGAG 95

RESULT 8
LOCUS A1112727 377 bp mRNA linear EST 01-AUG-1997

DEFINITION zn62b01.x1 Stratiagene muscle 937209 Homo sapiens cDNA clone
IMAGE:562729 5' similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);,
mRNA sequence.

ACCESSION A1112727
VERSION A112727.1 GI:1663860
KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 377)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissole, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE 97044478

JOURNAL MEDLINE

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 378
Insert Length: 450 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 356.

FEATURES

1..377
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:456019"

/db_xref="taxon:9606"
/clone="IMAGE:562729"
/clone_lib="Stratiagene muscle 937209"
/tissue_type="muscle"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skeletal muscle; Vector: p Bluescript SK-;
Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally.
Primer: Oligo dT. Skeletal muscle from patient with
malignant hyperthermia. Average insert size: 1.0 kb;
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGCGACGAG
3'-3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT 113 a 83 c 100 g 81 t

ORIGIN

Query Match 100.0%; Score 282; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 1,8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaccgagcttggagaagccttgaactctatcaltcagcgtctaccacaagtactcc 60
DB 23 ATGTGACCGAGCTGGAGAAAGCCTTGAACTCTATCATCGAGCTACCAACTACTCC 82
QY 61 ctgataaagggaattccatgcgcgtctacaggagatgacctgaagaattgtctagacc 120
DB 83 CTGATTAAGGGGAATTTCCATGCCCTTACAGGATGACCTGAAGAAATTCCTAGAGACC 142
QY 121 gagtgcctcagtatatcaggaaaagggtgcagcgtctgttcaagaagtgtatatac 180
DB 143 GAGTGTCTCTCACTATATATAGCAAAAAGGCTGACAGCTGTCTGTTCAAGAATTGGATATC 202
QY 181 aacactgatgtgcagtaacttccaggagttcctcattctgtgtatataaagtggcgtg 240
DB 203 AACACTGATGGTGGAGTTAACTTCCAGAGTTCTCATTTCTGGATTAAGATGGGCGCTG 262
QY 241 gcagcccaaaaaaagccatgagaagaagccacaagaagttag 282
DB 263 GCAGCCACAAAAAAGCCATGAAGAAAGCCACAAAGATGAG 304

RESULT 9

LOCUS

DEFINITION

zn50h04.x1 NCI-CGAP_HN7 Homo sapiens cDNA clone IMAGE:2754103 3'
similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);,
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 370.
Location/Qualifiers

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source
1. .380
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:2754103"
/clone_lib="NCI-CGAP_HN7"
/tissue_type="normal squamous epithelium, floor of mouth"
/lab_host="DH10B"
/Note="Vector: PAMPI0; cDNA made by oligo-dT priming.
Non-directionally cloned into the UDG sites of PAMPI0.
Size selected on agarose gel, average insert size 500 bp.
Primary library; non-amplified. cDNA Library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT      109 a      85 c      104 g      82 t
ORIGIN

Query Match      100.0%; Score 282; DB 9; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaccgagcttgagaaagccttgaacctatcatcgaagctccacaagttacc 60
Db 48 ATGTTGACCGAGCTGAGAAAGCCTTGAACCTATCATCGACGCTACCAAGTACTCC 107
QY 61 ctgataaagggaattccatgcgctctacagagatgaacctgaagaattgctagagacc 120
Db 108 CTGATTAAGGGGAATTTCCATGCCGCTCTACAGGGATGACCTGAAGAAATTGCTAGAGACC 167
QY 121 gaggtctctcgtatatacagaagaagggtgcagagctctggttcaagaagttggatatac 180
Db 168 GAGGTCTCTCGTATATCAGGAAAAAGGTCACACGCTGCTTCAAGAGATTGATATC 227
QY 181 aacactgatgtgcagtttaacttccagagagttctctatctgtgtgataagaatgggggtg 240
Db 228 AACACTGATGTGTCAGTTACTTCCAGAGATTCTCTATTCTGTGATTAAGATGGCGCTG 287
QY 241 gcagcccaaaaaaagccatgaagaagccacaaagatgag 282
Db 288 GCAGCCCAAAAAAGCCATGAAGAAAGCCACAAAGATGAG 329

RESULT 10
AM238239      384 bp      mRNA      linear      EST 13-DEC-1999
LOCUS      AM238239
DEFINITION      xp23405.x1 NCI-CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741193 3'
similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);, mRNA sequence.
ACCESSION      AM238239
VERSION      AM238239.1 GI:6570711
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 384)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Edward J. Shillito, Ph.D., Silvio Gutkind Ph.D.,
Chidhanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbfp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -400P from Gibco
High quality sequence stop: 367.
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FEATURES
source
Location/Qualifiers
1. .384
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:2741193"
/clone_lib="NCI-CGAP_HN10"
/tissue_type="carcinoma in situ from retromolar trigone"
/lab_host="DH10B"
/Note="Vector: PAMPI0; cDNA made by oligo-dT priming.
Non-directionally cloned into the UDG sites of PAMPI0.
Size selected on agarose gel, average insert size 500 bp.
Primary library; non-amplified. cDNA Library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT      113 a      85 c      105 g      81 t
ORIGIN

Query Match      100.0%; Score 282; DB 9; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaccgagcttgagaaagccttgaacctatcatcgaagctccacaagttacc 60
Db 46 ATGTTGACCGAGCTGAGAAAGCCTTGAACCTATCATCGAGCTTACCAAGTACTCC 105
QY 61 ctgataaagggaattccatgcgctctacagagatgaacctgaagaattgctagagacc 120
Db 106 CTGATTAAGGGGAATTTCCATGCCGCTCTACAGGGATGACCTGAAGAAATTGCTAGAGACC 165
QY 121 gaggtctctcgtatatacagaagaagggtgcagagctctggttcaagaagttggatatac 180
Db 166 GAGGTCTCTCGTATATCAGGAAAAAGGTCACACGCTGCTTCAAGAGATTGATATC 225
QY 181 aacactgatgtgcagtttaacttccagagagttctctatctgtgtgataagaatgggggtg 240
Db 226 AACACTGATGTGTCAGTTACTTCCAGAGATTCTCTATTCTGTGATTAAGATGGCGCTG 285
QY 241 gcagcccaaaaaaagccatgaagaagccacaaagatgag 282
Db 286 GCAGCCCAAAAAAGCCATGAAGAAAGCCACAAAGATGAG 327

RESULT 11
BF478287/c      384 bp      mRNA      linear      EST 05-DEC-2000
LOCUS      BF478287/c
DEFINITION      nae46908.x1 NCI-CGAP_HN16 Homo sapiens cDNA clone IMAGE:4115127 3'
similar to SW:S108_HUMAN P05109 CALGRANULIN A ;, mRNA sequence.
ACCESSION      BF478287
VERSION      BF478287.1 GI:11549114
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 384)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Edward J. Shillito, Ph.D., Chidhanok
Leethanakul
cDNA Library Preparation: D. Krizman & C. Leethanakul Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
info@image.llnl.gov
Seq primer: -400P from Gibco.
Location/Qualifiers
1. .384
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Query Match	100.0%	Score 282;	DB 10;	Length 384;
Best Local Similarity	100.0%;	Pred. No. 1.8e-66;		
Matches 282;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	atgttgaccggagctgagaaagaccttgaccctatcatctgagcgtctacccaagttacc	60
Db	367	ATGTTGACCGAGCTGGAAGAAACCTTGAACTCTATCATCTGAGCTTACCACAAAGTACTCC	308
QY	61	ctgataaaggaggaaattccatgycggtctacaaggatgacctgaaanaattgctagaagcc	120
Db	307	CTGATAAAGGGGGAATTTCCATGCCCTCTACAGAGGTGACTCGAAGAAATTTGCTAAGAGCC	248
QY	121	gagttcctcagtatatacgaagaagggttcagacgcgtgtgtctaaagagttgatactc	180
Db	247	GAGTCTCCTCATATATATAGGAAAAGGGTGCAGACGCTGTGTTCAAAAGATTGGATATTC	188
QY	181	aacactgtagtgcagttactctccaggagatctccattcttcgltgataaagatgggcgtg	240
Db	187	AACACTGATGCTGCAGTTAACTTCCAGGAGTTCCATCTTGATGATTAAGATGGCGCG	128
QY	241	gcagcccaaaaaaaagccatgaaagaagccacaagaagtgg	292
Db	127	GCAGCCCAAAAAAAGCCATGAAAGAAAGCCACAAGAGTGG	86

RESULT	12
LOCUS	AM238329
DEFINITION	AM238329 386 bp mRNA linear EST 13-DEC-1999
ACCESSION	xp21a08.x1 NCI-CGAP_HN10 Homo sapiens CDNA clone IMAGE:2740982 3'
VERSION	similar to gb:A12027_cds1 CALGRANULIN A (HUMAN); mRNA sequence.
KEYWORDS	AM238329 AM238329.1 GI:6570646
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D., Chidchanok Leelthanakul D.D.S., Michael Emmert-Buck M.D. Ph.D. CDNA Library Preparation: David B. Kitzman, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.llnl.gov/bbrp/image/image.html Seq primer: -40up from Clbco. Location/Qualifiers 1..386 /organism="Homo sapiens" /db_xref="taxon:9606"
FEATURES	
Source	

Query Match	100.0%	Score 282;	DB 9;	Length 386;
Best Local Similarity	100.0%	Pred. No. 1.8e-66;		
Matches 282; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	atgtttgacgcagcttgagaaagcccttgaaactatcacacgaagcttaccaagaatccc	60
Db	15	ATGTTGACCGAGCTGGAGAAACCTTGAACCTATCATCGAGCTTACCACAACTACTCC	74
QY	61	ctgataaaggaggaaattccatgcgcgtctacaaggatgaacctgaagaanaattgctagaagcc	120
Db	75	CTGATTAAGAGGGGAATTTCCATCCCTGTACAGAGATGACCTGAAMAATTTGCTAAGAGCC	134
QY	121	gagttctctcagtatataagaaagggttgaaagcgcctggttcaaaagcttgatactc	180
Db	135	GAGTCTCCTCACTATATACGAAAAAGGCTGACAGCTGTGTTTAAAGATGGATATTC	194
QY	181	aaactatgtgtgcagtttaacttccagaagatgcccatcttctgtatataaagtggcgtg	240
Db	195	AACACTGATGGTGCAAGTTAACTTCCAGGAGTTCCTCATTTCTGTATTAAGATGGGCGG	254
QY	241	gcagcccccacaaaaaagccatgaaagaagcccaagaaggttag	262
Db	255	GCAGGCCACAAAAAAGGCATGAAAGAAAGCCCAAAAGAGTAG	296

	RESULT#	13				
	LOCUS	AM080385/c				
	DEFINITION	AM080385	388 bp	mRNA	linear	EST 14-OCT-1999
	ACCESSION	x64e08.xl	NCI-CGAP_Esc2	Homo sapiens cDNA clone IMAGE:2610470	3'	
	VERSION	similar to gp:A12027_cds1 CALGRANDLIN A (HUMAN);		mRNA sequence.		
	KEYWORDS	AM080385	.1	GI:6035537		
	SOURCE	EST.				
	ORGANISM	human.				
		Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	REFERENCE	1	(bases 1 to 388)			
	AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.			
	TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL COMMENT		Unpublished (1997)				
	Contact:	Robert Strausberg, Ph.D.				
	Email:	cgapbs_r@mail.nih.gov				
	Tissue Procurement:	Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.				
	CNA Library Preparation:	Life Technologies, Inc.				
	CNA Library Arrayed by:	Greg Lennon, Ph.D.				
	DNA Sequencing by:	Washington University Genome Sequencing Center				
	Clone distribution:	NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNW at: www.bio.lnl.gov/bdrip/image/Image.html Seq primer: -40UP from Gibco				
	High quality sequence stop:	373.				
FEATURES		Location/Qualifiers				
SOURCE		1..388				
	/organism=	"Homo sapiens"				
	/db_xref=	"taxon:9606"				
	/clone=	"IMAGE:2610470"				

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/clone_lib="NCI-CGAP_Eso2"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B"
;note="Organ: esophagus; Vector: PCMV-SPORT6; Site_1: Salt
; Site_2: Not; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.1 kb. Life Technologies catalog
#: 11502-010"
BASE COUNT      84 a      102 c      86 g      116 t
ORIGIN

Query Match      100.0%; Score 282; DB 9; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgttgacgcagctgagaaagccttgaaactatcatcgacgcttaccacaagctacc 60
DB 352 ATGTTGACCGAGCTGGAGAAAGCCTTGAACTTATCATCGACGTTACCAAGTACTCC 293
OY 61 ctgataaagggaatttcctacgctcctacagagatgacctgaaagaattgctagaacc 120
DB 292 CTGATTAAGGGGAATTTCCATGCCGTACAGAGATGACCTGAAGAATTTGCTAGAGACC 233
OY 121 gaggttcctcaatatacaggaagaggtgcagacgtcttggttcaagaagttgatatc 180
DB 232 GAGTGTCTCCTCATATATCAGGAAAAAGGTCGACACGTCGTCAAGAGTTGATATC 173
OY 181 aacactgagtgtgcagtttaacttccagagatcctcattcttggtatagaatggcgctg 240
DB 172 AACACTGATGTGTGCGATTACTTCAGAGAGTTCTCTCATTTGGTGATTAAGATGGCGGTG 113
OY 241 gcagcccaaaaaaagccatgaagaagccacaagaagtag 282
DB 112 GCAGCCCAAAAAAGCCATGAGAAAGCCACAAAGAGTAG 71

RESULT 14      389 bp      mRNA      linear      EST 22-MAY-2000
AW873740
LOCUS      hg29ell.x1 NCI-CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120812 3'
DEFINITION similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);, mRNA sequence.
ACCESSION      AW873740
VERSION      AW873740.1 GI:8007793
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 389)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL      Tumor Gene Index
COMMENT      Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.lnl.gov
Seq primer: -40UP from GIBCO.

FEATURES
Source
1..389
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3120812"
/clone_lib="NCI-CGAP_Adr1"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: PCMV-SPORT6; Site_1:

```

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;note="Organ: heart; Vector: pRT73D (Pharmacia) with a
Not; Site_2: Salt; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.2 kb. Library
constructed by Life Technologies."
BASE COUNT      84 a      102 c      87 g      116 t
ORIGIN

Query Match      100.0%; Score 282; DB 9; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgttgacgcagctgagaaagccttgaaactatcatcgacgcttaccacaagctacc 60
DB 352 ATGTTGACCGAGCTGGAGAAAGCCTTGAACTTATCATCGACGTTACCAAGTACTCC 293
OY 61 ctgataaagggaatttcctacgctcctacagagatgacctgaaagaattgctagaacc 120
DB 292 CTGATTAAGGGGAATTTCCATGCCGTACAGAGATGACCTGAAGAATTTGCTAGAGACC 233
OY 121 gaggttcctcaatatacaggaagaggtgcagacgtcttggttcaagaagttgatatc 180
DB 232 GAGTGTCTCCTCATATATCAGGAAAAAGGTCGACAGCTGTGTTCAAGAGTTGATATC 173
OY 181 aacactgagtgtgcagtttaacttccagagatcctcattcttggtatagaatggcgctg 240
DB 172 AACACTGATGTGTGCGATTACTTCAGAGAGTTCTCTCATTTGGTGATTAAGATGGCGGTG 113
OY 241 gcagcccaaaaaaagccatgaagaagccacaagaagtag 282
DB 112 GCAGCCCAAAAAAGCCATGAGAAAGCCACAAAGAGTAG 71

RESULT 15      390 bp      mRNA      linear      EST 25-JUN-1996
W79564
LOCUS      Z076g11.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone
DEFINITION IMAGE:346628 5' similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);,
mRNA sequence.
ACCESSION      W79564
VERSION      W79564.1 GI:1390835
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 390)
AUTHORS      Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, K., Kucaba, T., Le, M., Lennon, G., Maita, M., Parsons, J.,
Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Watson,
R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLES      The WashU-Merck EST Project
JOURNAL      Unpublished (1995)
COMMENT      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: mbd.RGA+ET
High quality sequence stop: 375.

FEATURES
Source
1..390
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:1272003"
/db_xref="taxon:9606"
/clone="IMAGE:346628"
/clone_lib="Soares_fetal_heart_NbH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pRT73D (Pharmacia) with a

```

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TCTTACCAATCTGAAGTGGAGCGCGCCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT773 vector
(Pharmacia). Library went through one round of
normalization to a Col = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W.*

BASE COUNT 120 a 85 c 103 g 81 t 1 others
ORIGIN

Query Match 100.0%; Score 282; DB 10; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgttgaccgagctggggaagaccttgaactctatcatgagctctaccacaagtactcc 60
DB 35 ATGTTGACCGAGCTGGAGAAAGCCTTGAACTCTATCATCGACGCTTACCAAGTACTTC 94
QY 61 ctgataaagggaatttcacatgcgtctacagggatgacctgaagaattgctagagacc 120
DB 95 CTGATTAAGGGGGAATTTCATGCGCTCTACAGGATGACCTGAAGAAATTGCTAGAGACC 154
QY 121 gaggtctcagtatatcaaggaagaggtgcagacgtctggttcaagaagttgatatc 180
DB 155 GAGTGTCTCTCAGTATATCAGAGAAAGGTTGACAGCTCTGTTCAAGAGTTGGATATC 214
QY 181 aacactgatgtgcagtttaacttccagaggttcctcattctgtgtgataaagatgggcgtg 240
DB 215 AACACTGATGTTGCAATTAATTCCAGAGTTCCTCATCTCTGTTGATTAAGATGGGCGTGG 274
QY 241 gcaagcccaaaaaaagccatgaagaagccacaagaagtag 282
DB 275 GCAGCCCAAAAAAGCCATGAAGAAAGCCACAAAGAGTAG 316

Search completed: September 10, 2002, 06:07:54
Job time: 6630 sec

/protein_id="CAC16554.1"
/db_xref="GI:1128053"
/translation="MTLEKALNSIIDVHKYSILKGNFHAAYRDDLKULETECCQ
YIRKGAQVWKEKDINDGAVNQEFILIVIKGVAAHKSHESHEKE"

BASE COUNT 90 a 59 c 72 g 61 t

Query Match 100.0%; Score 282; DB 6; Length 282;
Best Local Similarity 100.0%; Pred. No. 6e-69;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 atgttaccgagctggagaagccttgaactatcatcagcgtctacacaagctacc 60
Db 1 ATGTTGACCGAGCTGGAGAAAGCCTTGACCTATCATCGACGCTCCACAACTACTCC 60
QY 61 ctgataaagggaattccatgcgctctcagaagatgacctgaagaattctgaagac 120
Db 61 CTGATTAAGGGGAATTTCCATGCCCTGACAGGATGACCTGAAGAAATTCCTAGAGAC 120
QY 121 gagtgcctcagatatacagaagaaggtgacagcgtctgttcaagaagtgtatc 180
Db 121 GAGTGTCCCTCAGTATATCATCGAGAAAAGGTGACAGACGCTGTGTTCAAAAGATTGATATC 180
QY 181 aacactgatgtgacgttaactcagagagttccctcatctgtgtataaagatggcgtg 240
Db 181 AACACTGATGTGTCAGTTAACTTCCAGAGTTCCTCATCTGTGATTAAGATGGCGGTG 240
QY 241 gtagcccaaaaaaacatgaagaagcccaagaagtag 282
Db 241 GCAGCCCAAAAAAGCCATGTAAGAACCAAAAGAGTAG 282

RESULT 2
LOCUS A12022 284 bp DNA linear PAT 11-JAN-1994
DEFINITION Macrophage migration inhibition factor (MRP-8).
ACCESSION A12022
VERSION A12022.1 GI:491243
KEYWORDS
SOURCE .
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 284)
AUTHORS Odink,K.G., Clerc,R., Cerletti,N., Brueggen,J., Tarcsay,L., Sorg,C.
and Wiesendanger,W.
TITLE Novel lymphokine related peptides
JOURNAL Patent: EP 0263072-A 6 06-APR-1988;
CIBA-GEIGY AG
FEATURES
source Location/Qualifiers
1..284
/organism="synthetic construct"
/db_xref="taxon:32630"

misc_difference 1
/note="n= a flanking DNA residue of 12 nucleotides or more
containing a promoter sequence".

gene 2..283
/gene="MRP-8"

CDS 2..283
/gene="MRP-8"
/codon_start=1
/transl_table=1
/protein_id="CAA0098.1"
/db_xref="GI:491244"
/translation="MTLEKALNSIIDVHKYSILKGNFHAAYRDDLKULETECCQ
YIRKGAQVWKEKDINDGAVNQEFILIVIKGVAAHKSHESHEKE"

misc_difference 284
/note="n= a flanking DNA residue of one or more
nucleotides or is absent"

BASE COUNT 90 a 59 c 72 g 61 t 2 others
ORIGIN

Query Match 100.0%; Score 282; DB 6; Length 284;
Best Local Similarity 100.0%; Pred. No. 6e-69;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 atgttaccgagctggagaagccttgaactatcatcagcgtctacacaagctacc 60
Db 2 ATGTTGACCGAGCTGGAGAAAGCCTTGACCTATCATCGACGCTCCACAACTACTCC 61
QY 61 ctgataaagggaattccatgcgctctcagaagatgacctgaagaattctgaagac 120
Db 62 CTGATTAAGGGGAATTTCCATGCCCTGACAGGATGACCTGAAGAAATTCCTAGAGAC 121
QY 121 gagtgcctcagatatacagaagaaggtgacagcgtctgttcaagaagtgtatc 180
Db 122 GAGTGTCCCTCAGTATATCATCGAGAAAAGGTGACAGACGCTGTGTTCAAAAGATTGATATC 181
QY 181 aacactgatgtgacgttaactcagagagttccctcatctgtgtataaagatggcgtg 240
Db 182 AACACTGATGTGTCAGTTAACTTCCAGAGTTCCTCATCTGTGATTAAGATGGCGGTG 241
QY 241 gtagcccaaaaaaacatgaagaagcccaagaagtag 282
Db 242 GCAGCCCAAAAAAGCCATGTAAGAACCAAAAGAGTAG 283

RESULT 3
LOCUS AR015927 408 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776348.
ACCESSION AR015927
VERSION AR015927.1 GI:3972204
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Selengut,J.D., Orme-Johnson,W.H., Dretler,S.P. and Asakura,H.
TITLE Mineral precipitation system and method for inhibiting mineral
precipitate formation
JOURNAL Patent: US 5776348-A 2 07-JUL-1998;
FEATURES
source Location/Qualifiers
1..408
/organism="unknown"

BASE COUNT 118 a 91 c 106 g 93 t
ORIGIN

Query Match 100.0%; Score 282; DB 6; Length 408;
Best Local Similarity 100.0%; Pred. No. 6.3e-69;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 atgttaccgagctggagaagccttgaactatcatcagcgtctacacaagctacc 60
Db 57 ATGTTGACCGAGCTGGAGAAAGCCTTGACCTATCATCGACGCTCCACAACTACTCC 116
QY 61 ctgataaagggaattccatgcgctctcagaagatgacctgaagaattctgaagac 120
Db 117 CTGATTAAGGGGAATTTCCATGCCCTGACAGGATGACCTGAAGAAATTCCTAGAGAC 176
QY 121 gagtgcctcagatatacagaagaaggtgacagcgtctgttcaagaagtgtatc 180
Db 177 GAGTGTCCCTCAGTATATCATCGAGAAAAGGTGACAGCTGTGTTCAAAAGATTGATATC 236
QY 181 aacactgatgtgacgttaactcagagagttccctcatctgtgtataaagatggcgtg 240
Db 237 AACACTGATGTGTCAGTTAACTTCCAGAGTTCCTCATCTGTGATTAAGATGGCGGTG 296
QY 241 gtagcccaaaaaaacatgaagaagcccaagaagtag 282
Db 297 GCAGCCCAAAAAAGCCATGTAAGAACCAAAAGAGTAG 338

RESULT 4

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193571      193571      418 bp      DNA      linear      PAT 01-DEC-1998
LOCUS       Sequence 15 from patent US 5731166.
ACCESSION  193571
VERSION    193571.1  GI:3938041
KEYWORDS
SOURCE     unknown.
ORGANISM   unknown.
REFERENCE  1 (bases 1 to 418)
AUTHORS    Geozzy, C., Simpson, R. John, and Lackmann, M.
TITLE      Recombinant production of chemotactic CP-10 polypeptides and
           therapeutic methods using them
JOURNAL    Patent: US 5731166-A 15 24-MAR-1998;
FEATURES   Location/Qualifiers
            source          1..418
                        /organism="unknown"
BASE COUNT 128 a      91 c      106 g      93 t
ORIGIN
Query Match      100.0%; Score 282; DB 6; Length 418;
Best Local Similarity 100.0%; Pred. No. 6,3e-69;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgttgaccgagctgagaagaagccttgaactctatcatcagcgtctaccacaagtactcc 60
    |||||||
DB 57 atgttgaccgagctgagaagaagccttgaactctatcagcgtctaccacaagtactcc 116
    |||||||
QY 61 ctgataaagggaattccatgcgcgtctcagaggaatgactcgaagaatctgataagacc 120
    |||||||
DB 117 ctgataaagggaattccatgcgcgtctcagaggaatgactcgaagaatctgataagacc 176
    |||||||
QY 121 gagtgccccagatatacagaagaagggtgcagacgtctgttcaagaagcttgatatac 180
    |||||||
DB 177 gagtgccccagatatacagaagaagggtgcagacgtctgttcaagaagcttgatatac 236
    |||||||
QY 181 aacactgatgtgagtaacttccagagagcttccatctcgtgtgataaagatggcgctg 240
    |||||||
DB 237 AACACTGATGTGTCAGTAACTTCACAGAGTTCCTCATCTGATGAAGATGGGCGTG 296
    |||||||
QY 241 gcaagcccaaaaaaagccatgaagaagcccaagaagatag 282
    |||||||
DB 297 GCAGCCACAAAAAAGCCATGAAGAACCCACAAAGAGTAG 338
    |||||||

RESULT 5
HSMRP8      418 bp      mRNA      linear      PRI 12-SEP-1993
LOCUS       Human mRNA for calcium-binding protein in macrophages (MRP-8)
DEFINITION  macrophage migration inhibitory factor (MIF)-related protein.
ACCESSION  X06234 Y00286
VERSION    X06234.1  GI:34772
KEYWORDS   calcium binding protein; cystic fibrosis antigen.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 418)
AUTHORS    Odink, K.
TITLE      Direct Submission
JOURNAL    Submitted (12-NOV-1987) Odink K., Ciba-Geigy, Dept. of
           Biotechnology, K 681-442, 4002 Basel, Switzerland
           2 (bases 1 to 418)
           Odink, K., Cerletti, N., Brugger, J., Clerc, R. G., Tarcsay, L.,
           Zwadlo, G., Gerhards, G., Schlegel, R., and Sorg, C.
           Two calcium-binding proteins in infiltrate macrophages of
           rheumatoid arthritis
JOURNAL    Nature 330 (6143), 80-82 (1987)
MEDLINE    88039099
COMMENT    MRP-8 protein is myeloid specific expressed in chronic
           inflammation; see X06233.
           The sequence of MRP-8 is identical to the sequence for the cystic

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fibrosis CCR1 antigen, with one exception (additional G at 292;
Y00278). This difference can reflect a natural variation in alleles
or could arise from a sequencing error. X06234 sequence was
confirmed for three independent cDNAs and for a chromosomal MRP-8
gene
(Lagasse E. and R.G.C., Mol. Cell. Biol., submitted).
FEATURES
source
1..418
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="peripheral blood mononuclear cells"
CDS
57..338
/note="MRP-8 (AA 1-93)"
/codon_start=1
/protein_id="CAA29580.1"
/db_xref="GI:34773"
/db_xref="SWISS-PROT:P05109"
/translation="MTLEKALNINSDYHYSLIKGFHAYRDLKILETCPO
YIRKQADWFKRIDINTGAVNFOEFLIVIKMGVAARKSHESHKE"

BASE COUNT 128 a      91 c      106 g      93 t
ORIGIN
Query Match      100.0%; Score 282; DB 9; Length 418;
Best Local Similarity 100.0%; Pred. No. 6,3e-69;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgttgaccgagctgagaagaagccttgaactctatcagcgtctaccacaagtactcc 60
    |||||||
DB 57 atgttgaccgagctgagaagaagccttgaactctatcagcgtctaccacaagtactcc 116
    |||||||
QY 61 ctgataaagggaattccatgcgcgtctcagaggaatgactcgaagaatctgataagacc 120
    |||||||
DB 117 ctgataaagggaattccatgcgcgtctcagaggaatgactcgaagaatctgataagacc 176
    |||||||
QY 121 gagtgccccagatatacagaagaagggtgcagacgtctgttcaagaagcttgatatac 180
    |||||||
DB 177 gagtgccccagatatacagaagaagggtgcagacgtctgttcaagaagcttgatatac 236
    |||||||
QY 181 aacactgatgtgagtaacttccagagagcttccatctcgtgtgataaagatggcgctg 240
    |||||||
DB 237 AACACTGATGTGTCAGTAACTTCACAGAGTTCCTCATCTGATGAAGATGGGCGTG 296
    |||||||
QY 241 gcaagcccaaaaaaagccatgaagaagcccaagaagatag 282
    |||||||
DB 297 GCAGCCACAAAAAAGCCATGAAGAACCCACAAAGAGTAG 338
    |||||||

RESULT 6
BC005928      423 bp      mRNA      linear      PRI 12-JUL-2001
LOCUS       Homo sapiens, S100 calcium-binding protein A8 (calgranulin A),
DEFINITION  clone MGC:14536 IMAGE:4246359, mRNA, complete cds.
ACCESSION  BC005928
VERSION    BC005928.1  GI:13543538
KEYWORDS   MGC.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 423)
AUTHORS    Strausberg, R.
TITLE      Direct Submission
JOURNAL    Submitted (02-APR-2001) National Institutes of Health, Mammalian
           Gene Collection (MGC), Cancer Genomics Office, National Cancer
           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
           USA
REMARK     NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT    Contact: MGC help desk
           Email: cgabs-remail.nih.gov
           Tissue Procurement: CLONTECH
           cDNA Library Preparation: CLONTECH Laboratories, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdexapil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAL Plate: 21 Row: c Column: 4
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 34772.

FEATURES

Location/Qualifiers

1..423
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="MGC:14536 IMAGE:4246359"
 /tissue_type="Skeletal Muscle"
 /clone_id="NH_MGC_81"
 /lab_host="DH10b"
 /note="Vector: pDNR-LIB"
 56..337
 /codon_start=1
 /product="S100 calcium-binding protein A8 (calgranulin A)"
 /protein_id="AAH05928.1"
 /db_xref="GI:13543539"
 /translation="MLTELEKALNSIIDVYHKSLIKGNFHAVYRDDLKLETECPD YIRKKGADVWFREKIDINTDGAVNFQEFILIVIMGVAAHKSHSHKE"

CDS

BASE COUNT 135 a 91 c 106 g 91 t
 ORIGIN

Query Match 100.0%; Score 282; DB 9; Length 423;
 Best Local Similarity 100.0%; Pred. No. 6.3e-69;

Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttgaccgagctggaagaagccttgaactctatcatcagcgtctcaccaagctacc 60
 |||||||
 Db 56 ATGTTGACCGCGCTGAGAAAGCCTGAACCTCATCATCAGCGTCCACAGTACTCC 115
 QY 61 ctgataaagggaattccatcgctctacagagatgacttgaaagaattgctagaagc 120
 |||||||
 Db 116 CTGATAAAGGGGAATTTCCATGCGCTTACAGGAGATGACTGAAGAAATTTGTAAGACC 175
 QY 121 gagtgtccctcagatatacgaagaaagggtcgaagcgtcgtgtccaaagagttgatatc 180
 |||||||
 Db 176 GAGTGTCTCAGTATATCAGAGAAAGCGTGCAGACGTCGTGTTCAAAAGATTGGATATC 235
 QY 181 aacactgatgtgcagtttaacttccagagagttccctcatctctgtatgaagatggcgctg 240
 |||||||
 Db 236 AACACTGATGTCAGTAACTTCCAGAGAGTTCCTCATCTGCTGATAAAGATGGCGGTG 295
 QY 241 gcaagcccaaaaaaagccatgaagaagccacaaagaagtag 282
 |||||||
 Db 296 GCAGCCCAAAAAAAGCCATGAAGAAAGCCACAAGAGTAG 337

RESULT 7
 LOCUS A12025 485 bp mRNA linear PAT 11-JAN-1994
 DEFINITION Macrophage migration inhibition factor (MRP-14) cDNA from mRNA of a human mononuclear leukocyte (formula v).
 ACCESSION A12025
 VERSION A12025.1 GI:491247
 KEYWORDS
 SOURCE
 ORGANISM
 ORGANISM synthetic construct.
 ORGANISM synthetic construct.
 ORGANISM artificial sequence.
 ORGANISM 1 (bases 1 to 485)
 ORGANISM Odink, K.G., Clerc, R., Cerletti, N., Brueggem, J., Tarascy, L., Sorg, C. and Wiesendanger, W.
 ORGANISM Novel lymphokine related peptides

JOURNAL Patent: EP 0263072-A 10 06-APR-1988;
 CIBA-GEIGY AG

FEATURES

Location/Qualifiers

1..485
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 124..405
 /gene="MRP-8"
 124..405
 /gene="MRP-8"
 /codon_start=1
 /transl_table=1
 /protein_id="CAA01000.1"
 /db_xref="GI:491248"
 /translation="MLTELEKALNSIIDVYHKSLIKGNFHAVYRDDLKLETECPD YIRKKGADVWFREKIDINTDGAVNFQEFILIVIMGVAAHKSHSHKE"

CDS

BASE COUNT 152 a 106 c 114 g 113 t
 ORIGIN

Query Match 100.0%; Score 282; DB 6; Length 485;
 Best Local Similarity 100.0%; Pred. No. 6.4e-69;

Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttgaccgagctggaagaagccttgaactctatcatcagcgtctcaccaagctacc 60
 |||||||
 Db 124 ATGTTACCGAGCTGAGAAAGCCTTGAACCTCATCATCAGCGTCTACACCAAGTACTCC 183
 QY 61 ctgataaagggaattccatcgctctacagagatgacttgaaagaattgctagaagc 120
 |||||||
 Db 184 CTGATAAAGGGGAATTTCCATGCGCTTACAGGAGATGACTGAAGAAATTTGCTAGAGACC 243
 QY 121 gagtgtccctcagatatacgaagaaagggtcgaagcgtcgtgtccaaagagttgatatc 180
 |||||||
 Db 244 GAGTGTCTCAGTATATCAGAGAAAGCGTGCAGACGTCGTGTTCAAAAGATTGGATATC 303
 QY 181 aacactgatgtgcagtttaacttccagagagttccctcatctctgtatgaagatggcgctg 240
 |||||||
 Db 304 AACACTGATGTCAGTAACTTCCAGAGAGTTCCTCATCTGCTGATAAAGATGGCGGTG 363
 QY 241 gcaagcccaaaaaaagccatgaagaagccacaaagaagtag 282
 |||||||
 Db 364 GCAGCCCAAAAAAAGCCATGAAGAAAGCCACAAGAGTAG 405

RESULT 8
 LOCUS AX188193 2329 bp DNA linear PAT 06-AUG-2001
 DEFINITION Sequence 3888 from Patent WO0142467.
 ACCESSION AX188193
 VERSION AX188193.1 GI:15139666
 KEYWORDS
 SOURCE
 ORGANISM human.

ORGANISM Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2329)
 TITLE Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
 Genes, compositions, kits, and methods for identification,
 assessment, prevention, and therapy of cervical cancer
 Patent: WO 0142467-A 3888 14-JUN-2001;
 Millennium Predictive Medicine, Inc. (US)

FEATURES
 Location/Qualifiers

1..2329
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 715 a 398 c 509 g 707 t
 ORIGIN

Query Match 98.7%; Score 278.4; DB 6; Length 2329;
 Best Local Similarity 99.6%; Pred. No. 7.7e-68;
 Matches 279; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gttgaccgagctggagaaagccttgaactatcatcagcgtctacacaaagtactcc 62
|||||
Db 51 GTTGAACCGAGCTGGAGAAAGCTTGAACCTATCATCATGAGCTGTACCAAGTACTCCCT 110
QY 63 gataaagggaatttcacgtccgtctacagggaatgacccgaagaattgtctgaagccga 122
|||||
Db 111 GATTAAGGGGAATTTCCATCCGCTTACAGAGTACCTGAAATAATTCCTGAGACCCA 170
QY 123 gttcctcagatatacagagaaaggttcgaagcgtctgttcaaaagtgtgatalcaaa 182
|||||
Db 171 GTGCTCAGATATATCAGAAAAAGGTGACAGCTGTGTTCAAGAGTTGATATCA 230
QY 183 cactgagtggtgacgttactcagagagttccattccgttgatgaataagtggtgac 242
|||||
Db 231 CACTGATGtGtGAGTACTCTCTGAGTTCCTCATTCGTGATTAAGATGAGTGGTGC 290
QY 243 agccacacaaagccatgaagaagccacaaagagtag 282
|||||
Db 291 AGCCACAAAAAGCCATGAGAGCCACAAAGAGTAG 330

RESULT 9
HSCFANT 420 bp mRNA linear PRI 12-SEP-1993
LOCUS HSCFANT
DEFINITION Human mRNA for cystic fibrosis antigen (CFAG).
ACCESSION Y00278
VERSION Y00278.1 GI:29887
KEYWORDS calcium binding protein; cystic fibrosis antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 420)
Dorin,S.R.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1987) S. R. Dorin, Clinical and Population
MEDLINE Cytogenetics Unit, MRC, Western General Hospital, Crewe Road,
Edinburgh, Scotland, Great Britain
REFERENCE 2 (bases 1 to 420)
Dorin,J.R., Novak,M., Hall,R.E., Brock,D.J., Secher,D.S. and van
Heijningen,V.
TITLE A clue to the basic defect in cystic fibrosis from cloning the CF
JOURNAL Nature 326 (6113), 614-617 (1987)
MEDLINE 87173041

FEATURES
source Location/Qualifiers

CDS
52..336
/note="CFAG (AA 1-94)"
/codon_start=1
/protein_id="CAA68390.1"
/db_xref="GI:29887"
/db_xref="SWISS-PROT:P05109"
/translation="MTELEKALNSIIIVYHKYSLIKNFPAVYVDLKKLLETCRO
YIRKKADYVKEELDINTDGANVPODFLLIVYKMGWOTKAKMKATKSS"
misc_feature 85..175
/note="non-EF-hand calcium binding site"
misc_feature 199..289
/note="EF-hand calcium binding site"

BASE COUNT 138 a 90 c 101 g 90 t 1 others
ORIGIN

Query Match 95.7%; Score 270; DB 9; Length 420;
Best Local Similarity 99.6%; Pred. No. 1.5e-65;
Matches 281; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 atgttaccgagctggagaaagccttgaactatcatcagcgtctacacaaagtactcc 60
|||||
Db 52 ATGTTGACCGAGCTGGAGAAAGCTTGAACCTATCATCATGAGCTGTACCAAGTACTCC 111
QY 61 ctgtataagggaatttcacgtccgtctacagggaatgacccgaagaattgtctgaagcc 120
|||||
Db 112 CTGATTAAGGGGAATTTCCATCCGCTTACAGAGTACCTGAAATAATTCCTGAGACCC 171
QY 121 gatttccatagatatacagagaaaggttcgaagcgtctgttcaaaagtgtgatalc 180
|||||
Db 172 GAGTGTCTCAGATATATCAGAAAAAGGTGACAGCTGTGTTCAAGAGTTGATATC 231
QY 181 aacactgattgttcagttactccagagagttccattccgttgatgaataagtggtgac 240
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Db 232 AACACTGATGtGAGTACTCTCTGAGAGTTCCTCATTCGTGATTAAGATGAGGCTG 290
QY 241 gcagccacacaaagccatgaagaagccacaaagagtag 282
|||||
Db 291 GCAGCCACAAAAAGCCATGAGAGCCACAAAGAGTAG 332

RESULT 10
AX184529 573 bp DNA linear PAT 06-AUG-2001
LOCUS AX184529
DEFINITION Sequence 224 from Patent WO0142467.
ACCESSION AX184529
VERSION AX184529.1 GI:15135885
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 573)
Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patient: WO 0142467-A 224 14-JUN-2001,
MEDLINE Millennium Predictive Medicine, Inc. (US)

FEATURES
source Location/Qualifiers
1..573
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 173 a 109 c 154 g 137 t
ORIGIN

Query Match 81.7%; Score 230.4; DB 6; Length 573;
Best Local Similarity 99.6%; Pred. No. 2.3e-54;
Matches 231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 caagtactccctgataaagggaatttcacgtccgtctacagagatgacctgaagaatt 110
|||||
Db 10 CAGGTACTCCCTGATTAAGGGGAATTTCCATCCGCTTACAGAGATGACTTAAGAAATT 69
QY 111 gctagagaccgagtgctctcagatatacagagaaaggttcgaagcgtctgttcaaga 170
|||||
Db 70 GCTGAGAACACGAGAGTCTCATGATATCAGAAAAAGGTGACAGCTGTGTTCAAGA 129
QY 171 gttgataataaacctgattgttcagttactccagagagttccattccgttgatgaata 230
|||||
Db 130 GTTGATATCAACACGATGTCAGTTAATTCTTCAGAGATTCTCATTCGTGATTA 189
QY 231 gatggcgtgacgcccacacaaagccatgaagaagccacaaagagtag 282
|||||
Db 190 GATGGCGGTGGACGCCACAAAAAGCCATGAAAGAACCCACAAAGAGTAG 241

RESULT 11
AX186496 497 bp DNA linear PAT 06-AUG-2001
LOCUS AX186496
DEFINITION Sequence 2191 from Patent WO0142467.
ACCESSION AX186496
VERSION AX186496.1 GI:15137931

Query Match	77.4%	Score 218.4	DB 6	Length 598
Best Local Similarity	99.1%	Pred. No. 5,5e-51		
Matches 230	Conservative 0	Mismatches 1	Indels 1	Gaps 1
OY	51	caagtaactccctgataaagggaatttcctcatgcgctttacagsgatgtaactggaagaatt	110	
Db 1	12	CAGGTACTCTCCCTG-TAAAGGGGATTTTCAGTCCGCTGTACAGGGGATATACCTCGAAGAAATT	70	

RESULT	14				
LOCUS	AX187557				
DEFINITION	AX187557	381 bp	DNA		linear
ACCESSION	Sequence 3252 from Patent WO0142467.				
VERSION	AX187557				
KEYWORDS	AX187557.1	GI:15139019			
SOURCE					
ORGANISM	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 381)				
AUTHORS	Schlegel,R., Deeds,J., Berger,A. and Zhao,X.				
TITLE	Genes, compositions, kits and methods for identification,				

JOURNAL
assessment, prevention, and therapy of cervical cancer
Patent: WO 0142467-A 3252 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)

FEATURES
Source
1. .381
Location/Qualifiers

BASE COUNT 116 a 78 c 90 g 97 t
ORIGIN

Query Match 70.6%; Score 199; DB 6; Length 381;
Best Local Similarity 96.6%; Pred. No. 1.5e-45;
Matches 225; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 51 caagactccctgataaagggaattccatgcccgtctacaggaatgacctaagaatt 110
|||
Db 10 CAGGTACTCCCTGATTAAGGGGAATTTCACGCGTCTACAGGATGACCTGAAGAAATT 69
QY 111 gctagaagaccgagtgctcctcagtatatacagaaagaagtgacgctcgtgtcaaga 170
|||
Db 70 GCTAAGAGACCGAGTGTCTCTCAGTATCAGAGAAAAGGTCAGACGCTGTGTTCAAGA 129
QY 171 gttgataatcaacactgattggtcagtttaacttccaggaagttcctcattctgtgataa 230
|||
Db 130 GTTGATATCAACACTGATGTCAGTTAACTTC--AGGAGTCTCATCTGTGTGATATA 187
QY 231 gatggg-cgtggcagcccaaaaaaagccatgaagaagccaagaagtag 282
|||
Db 188 GATGGGCGGTGGCAGCCACAAAAGCCATGAAGAAAGCCACAAAGAGTAG 240

RESULT 15
AX184691 512 bp DNA linear PAT 06-AUG-2001
LOCUS AX184691
DEFINITION Sequence 386 from Patent WO0142467.
ACCESSION AX184691
VERSION AX184691.1 GI:15136053
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 512)
Schlegel, R., Deeds, J., Berger, A., and Zhao, X.
Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 0142467-A 386 14-JUN-2001;
JOURNAL Millennium Predictive Medicine, Inc. (US)
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Db 204 GATGGGCGGTGGCAGCCACAAAAGCCATGAAGAAAGCCACAAAGAGTAG 256

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